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(54) **HUMAN ADAMTS-1 PROTEIN, GENE CODING FOR THE SAME, PHARMACEUTICAL COMPOSITION, AND METHOD FOR IMMUNOLOGICALLY ASSAYING HUMAN ADAMTS-1 PROTEIN**

(57) A human ADAMTS- protein, a gene coding for the same, a pharmaceutical composition containing the protein as the active ingredient, and a method for immunologically assaying a human ADAMTS-1 protein. The protein can lower the number of leukocytes and thrombocytes and at the same time can increase the number of erythrocytes.

EP 1 004 674 A1

Description

TECHNICAL FIELD

- 5 [0001] The present invention relates to a human ADAMTS-1 protein, a gene encoding the same, a pharmaceutical composition, and a method for immunologically analyzing the human ADAMTS-1 protein.

BACKGROUND ART

- 10 [0002] A mouse ADAMTS (A disintegrin and metalloproteinase with thrombospondin motifs)-1 gene has been cloned as a cDNA from a mouse colon cancer cell which induces cancer cachexia when transplanted to a mouse. The mouse ADAMTS-1 protein encoded by the gene is a unique protein containing a matrix metalloproteinase domain, a disintegrin domain, and three thrombospondin domains [J. Biol. Chem., 272, 556-562 (1997)]. The physiological functions of the mouse ADAMTS-1 protein has not been reported, but there have been reports of each individual functional domain contained therein.

[0003] For example, a snake venom disintegrin belongs to a family of proteins which are rich in cysteine, and exhibit an anticoagulant activity [Semin. Hematol., 31, 289-300 (1994)].

- [0004] Further, for example, an ADAM (A disintegrin and metalloproteinase) family is known as a protein family containing a matrix metalloproteinase domain and a disintegrin domain [Nature, 377, 652-656 (1995); Nature Genet., 5, 151-157 (1993); Nature, 356, 248-252 (1992)]. Examples of known ADAM family proteins are fertilin, epidermal apical protein, cyritestin, MDC (metalloprotease-like, disintegrin-like and cysteine-rich protein), meltrin, MS2, and metargidin [Nature, 377, 652-656 (1995); Nature Genet. 5, 151-157 (1993); Nature, 356, 248-252 (1992); Biochem. J., 286, 671-675 (1992); Dev. Growth. Differ., 36, 49-58 (1994); Int. Immunol., 2, 585-591 (1990); J. Biol. Chem., 271, 4593-4596 (1996)].

- 25 [0005] It was reported that fertilin is involved in an integrin-mediated sperm-egg binding [Nature, 356, 248-252 (1992)], and meltrin is involved in a myotube formation [Nature, 377, 652-656 (1995)]. MDC expressed mainly in a central nervous system is a candidate as a suppresser against a human breast cancer [Nature Genet. 5, 151-157 (1993)], and MS2 serves as a macrophage antigen [Int. Immunol., 2, 585-591 (1990)]. However, little have been known about the physiological roles of these ADAM family proteins.

- 30 [0006] The mouse ADAMTS-1 protein contains a matrix metalloproteinase domain and a disintegrin domain, and therefore belongs to the ADAM family. However, the mouse ADAMTS-1 protein is different from other known ADAM family proteins in that it further contains thrombospondin domains.

- [0007] As mentioned, the ADAM family proteins have various kinds of activities such as the involvement of bone or muscle metabolism, suppression of cancer growth, or fertilization, and the thrombospondin exhibits an action to inhibit vascularization and suppresses cancer. Therefore, it is expected that the mouse ADAMTS-1 protein will exhibit unique physiological functions.

- [0008] The inventors of the present invention attempted to isolate the corresponding human ADAMTS-1 protein. Accordingly, the present inventors designed and prepared various probes on the basis of the base sequence of the known mouse ADAMTS-1 gene, and carried out plaque hybridizations with a human kidney cDNA library so as to obtain a human ADAMTS-1 gene, but a desired gene was not obtained. Then, the present inventors designed and prepared various primers on the basis of the base sequence of the known mouse ADAMTS-1 gene, and carried out PCRs, using the human kidney cDNA library as templates under ordinary conditions, so as to obtain the desired gene, but did not succeed.

- 45 [0009] Thereafter, the present inventors carried out a PCR of the human kidney cDNA library, using the same primers, but under conditions milder than those ordinarily used, more particularly, an annealing temperature is set lower than an ordinary temperature, and the inventors successfully obtained a novel human ADAMTS-1 gene. The resulting gene was then, expressed in E. coli, and the biological activities of the recombinant human ADAMTS-1 protein were examined. Surprisingly, it was found that the novel human ADAMTS-1 protein can decrease the numbers of leukocytes and platelets, and at the same time, increase the number of erythrocytes. Such activities in influencing hematopoietic functions cannot be expected from the structure of the mouse ADAMTS-1 gene which was used as the basis in designing the primers, or from the functions of domains contained in the human ADAMTS-1 protein. The present invention is based on the above findings.

DISCLOSURE OF INVENTION

- 55 [0010] The present invention relates to a protein characterized by containing an amino acid sequence of SEQ ID NO: 1:

EP 1 004 674 A1

Met Asp Ile Cys Arg Ile Arg Leu Arg Lys Lys Arg Phe Val Ser Ser
5 Pro Arg Tyr Val Glu Thr Met Leu Val Ala Asp Gln Ser Met Ala Glu
Phe His Gly Ser Gly Leu Lys His Tyr Leu Leu Thr Leu Phe Ser Val
Ala Ala Arg Leu Tyr Lys His Pro Ser Ile Arg Asn Ser Val Ser Leu
10 Val Val Val Lys Ile Leu Val Ile His Asp Glu Gln Lys Gly Pro Glu
Val Thr Ser Asn Ala Ala Leu Thr Leu Arg Asn Phe Cys Asn Trp Gln
15 Lys Gln His Asn Pro Pro Ser Asp Arg Asp Ala Glu His Tyr Asp Thr
Ala Ile Leu Phe Thr Arg Gln Asp Leu Cys Gly Ser Gln Thr Cys Asp
20 Thr Leu Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ser Arg Ser
Cys Ser Val Ile Glu Asp Asp Gly Leu Gln Ala Ala Phe Thr Thr Ala

EP 1 004 674 A1

His Glu Leu Gly His Val Phe Asn Met Pro His Asp Asp Ala Lys Gln
 Cys Ala Ser Leu Asn Gly Val Asn Gln Asp Ser His Met Met Ala Ser
 Met Leu Ser Asn Leu Asp His Ser Gln Pro Trp Ser Pro Cys Ser Ala
 Tyr Met Ile Thr Ser Phe Leu Asp Asn Gly His Gly Glu Cys Leu Met
 Asp Lys Pro Gln Asn Pro Ile Gln Leu Pro Gly Asp Leu Pro Gly Thr
 Leu Tyr Asp Ala Asn Arg Gln Cys Gln Phe Thr Phe Gly Glu Asp Ser
 Lys His Cys Pro Asp Ala Ala Ser Thr Cys Ser Thr Leu Trp Cys Thr
 Gly Thr Ser Gly Gly Val Leu Val Cys Gln Thr Lys His Phe Pro Trp
 Ala Asp Gly Thr Ser Cys Gly Glu Gly Lys Trp Cys Ile Asn Gly Lys
 Cys Val Asn Lys Thr Asp Arg Lys His Phe Asp Thr Pro Phe His Gly
 Ser Trp Gly Pro Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly
 Gly Gly Val Gln Tyr Thr Met Arg Glu Cys Asp Asn Pro Val Pro Lys
 Asn Gly Gly Lys Tyr Cys Glu Gly Lys Arg Val Arg Tyr Arg Ser Cys
 Asn Leu Glu Asp Cys Pro Asp Asn Asn Gly Lys Thr Phe Arg Glu Glu
 Gln Cys Glu Ala His Asn Glu Phe Ser Lys Ala Ser Phe Gly Ser Gly
 Pro Ala Val Glu Trp Ile Pro Lys Tyr Ala Gly Val Ser Pro Lys Asp
 Arg Cys Lys Leu Ile Cys Gln Ala Lys Gly Ile Gly Tyr Phe Phe Val
 Leu Gln Pro Lys Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser Thr
 Ser Val Cys Val Gln Gly Gln Cys Val Lys Ala Gly Cys Asp Arg Ile
 Ile Asp Ser Lys Lys Lys Phe Asp Lys Cys Gly Val Cys Gly Gly Asn
 Gly Ser Thr Cys Lys Lys Ile Ser Gly Ser Val Thr Ser Ala Lys Pro
 Gly Tyr His Asp Ile Val Thr Ile Pro Thr Gly Ala Thr Asn Ile Glu
 Val Lys Gln Arg Asn Gln Arg Gly Ser Arg Asn Asn Gly Ser Phe Leu
 Ala Ile Lys Ala Ala Asp Gly Thr Tyr Ile Leu Asn Gly Asp Tyr Thr
 Leu Ser Thr Leu Glu Gln Asp Ile Met Tyr Lys Gly Val Val Leu Arg
 Tyr Ser Gly Ser Ser Ala Ala Leu Glu Arg Ile Arg Ser Phe Ser Pro

Leu Lys Glu Pro Leu Thr Ile Gln Val Leu Thr Val Gly Asn Ala Leu
 5 Arg Pro Lys Ile Lys Tyr Thr Tyr Phe Val Lys Lys Lys Lys Glu Ser
 Phe Asn Ala Ile Pro Thr Phe Ser Ala Trp Val Ile Glu Glu Trp Gly
 10 Glu Cys Ser Lys Ser Cys Glu Leu Gly Trp Gln Arg Arg Leu Val Glu
 Cys Arg Asp Ile Asn Gly Gln Pro Ala Ser Glu Cys Ala Lys Glu Val
 Lys Pro Ala Ser Thr Arg Pro Cys Ala Asp His Pro Cys Pro Gln Trp
 15 Gln Leu Gly Glu Trp Ser Ser Cys Ser Lys Thr Cys Gly Lys Gly Tyr
 Lys Lys Arg Ser Leu Lys Cys Leu Ser His Asp Gly Gly Val Leu Ser
 20 His Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Phe Ile Asp Phe
 Cys Thr Leu Thr Gln Cys Ser.

25 [0011] Further, the present invention relates to the variation of proteins which are equivalent to the protein containing the amino acid sequence of SEQ ID NO: 1.

[0012] Further, the present invention relates to a protein characterized by containing a matrix metalloproteinase domain, a disintegrin domain, and a thrombospondin domain, except for a mouse ADAMTS-1 protein.

30 [0013] Further, the present invention relates to a gene characterized by encoding the above novel proteins.

[0014] Further, the present invention relates to a vector characterized by containing the above gene.

[0015] Further, the present invention relates to a transformant characterized by being transformed by the above vector.

35 [0016] Further, the present invention relates to a pharmaceutical composition characterized by comprising (1) the protein containing the amino acid sequence of SEQ ID NO: 1, (2) the variation functionally equivalent to the protein containing the amino acid sequence of SEQ ID NO: 1, or (3) the protein containing a matrix metalloproteinase domain, a disintegrin domain, and a thrombospondin domain.

[0017] Further, the present invention relates to an immunologically reactive substance (such as a polyclonal antibody or a monoclonal antibody, or an antibody fragment thereof, or an antiserum) characterized by nature of being capable of specifically reacting with the novel proteins.

40 [0018] Further, the present invention relates to a method for immunologically analyzing the human ADAMTS-1 protein, characterized in that a sample is brought into contact with the immunologically reactive substance, and a complex of the human ADAMTS-1 protein and the immunologically reactive substance is detected.

45 [0019] Further, the present invention relates to a method for analyzing an mRNA of the human ADAMTS-1 protein, characterized in that a sample is brought into contact with a polynucleotide containing a base sequence complementary to that of the mRNA of the human ADAMTS-1 protein consisting of the amino acid sequence of SEQ ID NO: 1, and a complex of the mRNA of the human ADAMTS-1 protein and the gene is detected.

[0020] Further, the present invention relates to a method for extracorporeally detecting an immunological state, characterized by analyzing the human ADAMTS-1 protein or the mRNA thereof.

50 [0021] Further, the present invention relates to an agent for analyzing an immunological state, characterized by containing the immunologically reactive substance capable of immunologically reacting the human ADAMTS-1 protein or the polynucleotide containing the base sequence complementary to that of the mRNA of the human ADAMTS-1 protein.

BRIEF DESCRIPTION OF DRAWINGS

[0022]

- 5 Figure 1 shows the results of an electrophoresis of a Flag. 1 DNA fragment produced by a PCR.
 Figure 2 shows a homology between the mouse ADAMTS-1 gene and the Flag. 1 DNA fragment.
 Figure 3 shows results of dot hybridization of the Flag. 1 DNA fragment.
 Figure 4 shows results of an electrophoresis of a Flag. 2 DNA fragment produced by a RACE.
 Figure 5 shows a homology in base sequences of the bases 1 to 480 in the human ADAMTS-1 gene and the mouse
 10 ADAMTS-1 gene.
 Figure 6 shows a homology in base sequences of the bases 481 to 960 in the human ADAMTS-1 gene and the
 mouse ADAMTS-1 gene.
 Figure 7 shows a homology in base sequences of the bases 961 to 1440 between the human ADAMTS-1 gene and
 the mouse ADAMTS-1 gene.
 15 Figure 8 shows a homology in base sequences of the bases 1441 to 1920 between the human ADAMTS-1 gene
 and the mouse ADAMTS-1 gene.
 Figure 9 shows a homology in base sequences of the bases 1921 to 2184 between the human ADAMTS-1 gene
 and the mouse ADAMTS-1 gene.
 Figure 10 shows a homology in amino acid sequences of the amino acids 1 to 240 between the human ADAMTS-
 20 1 protein and the mouse ADAMTS-1 protein.
 Figure 11 shows a homology in amino acid sequences of the amino acids 241 to 510 between the human
 ADAMTS-1 protein and the mouse ADAMTS-1 protein.
 Figure 12 shows a homology in amino acid sequences of the amino acids 511 between 727 in the human
 ADAMTS-1 protein and the mouse ADAMTS-1 protein.
 25 Figure 13 shows results of an electrophoresis of a full-length cDNA of the human ADAMTS-1 gene of the present
 invention, the cDNA being produced by a PCR.
 Figure 14 schematically illustrates a structure of plasmid pG/ADAMTS-1 of the present invention.
 Figure 15 shows results of an electrophoresis of a transformant transformed by the plasmid pG/ADAMTS-1.
 Figure 16 shows results of an electrophoresis of a GST-human ADAMTS-1 fusion protein.
 30 Figure 17 provides graphs showing effects on the numbers of blood cells when the GST-human ADAMTS-1 fusion
 protein is intravenously administered to a mouse in a single dosage.

BEST MODE FOR CARRYING OUT THE INVENTION

- 35 [0023] The present invention will be explained in detail hereinafter.
 [0024] The human ADAMTS-1 protein of the present invention is a novel protein consisting of 727 amino acid res-
 idues; that is, consisting of the amino acid sequence of SEQ ID NO: 1. As shown in Figs. 10 to 12, the human ADAMTS-
 1 protein of the present invention contains a matrix metalloproteinase (hereinafter sometimes referred to as "MMP")
 domain consisting of the 12th to 230th amino acid residues counting from the N-terminal amino acid residue, methio-
 40 nine; a disintegrin (hereinafter sometimes referred to as "DI") domain consisting of the 235th to 305th amino acid resi-
 dues; and three thrombospondin (hereinafter sometimes referred to as "TSP") domains consisting of the 322nd to
 372nd, 618th to 664th, and 672nd to 727th amino acid residues. The human ADAMTS-1 protein contains many
 arginines and lysines, which are basic amino acids, in a C-terminal region. Therefore, it is believed that the human
 ADAMTS-1 protein interacts with sulfated polysaccharide molecules, such as heparin or heparan sulfate, in blood.
 45 [0025] The novel protein according to the present invention includes the protein containing the amino acid
 sequence of SEQ ID NO: 1; and a variation functionally equivalent to the protein containing the amino acid sequence
 of SEQ ID NO: 1 (hereinafter sometimes referred to as a "human ADAMTS-1 protein variation"). The term "human
 ADAMTS-1 protein variation" as used herein means a protein having an amino acid sequence wherein one or more
 (particularly one or several) amino acids are deleted in, changed in, or inserted to the amino acid sequence of the
 50 human ADAMTS-1 protein, that is, the amino acid sequence of SEQ ID NO: 1, and exhibiting activities of the human
 ADAMTS-1 protein. A preferable human ADAMTS-1 protein variation has a 92% or more homology in the amino acid
 sequence with the human ADAMTS-1 protein. The human ADAMTS-1 protein variation includes a fragment which is a
 part of the protein containing the amino acid sequence of SEQ ID NO: 1 and exhibits the activities of the human
 ADAMTS-1 protein; and a fragment which is a part of another human ADAMTS-1 protein variation and exhibits the
 55 activities of the human ADAMTS-1 protein.
 [0026] The term "human ADAMTS-1 activity" as used herein means an activity to decrease the numbers of leuko-
 cytes and platelets, and at the same time, increase the number of erythrocytes.
 [0027] Further, the novel protein of the present invention includes a protein containing a matrix metalloproteinase

domain, a disintegrin domain, and a thrombospondin domain (hereinafter sometimes referred to as an "ADAMTS protein"). However, the mouse ADAMTS-1 protein is not included in the novel protein of the present invention.

[0028] The term "matrix metalloproteinase domain" as used herein means a domain containing an amino acid sequence having a 50% or more (preferably 95% or more) homology with the amino acid sequence of the matrix metalloproteinase domain in the human ADAMTS-1 protein, i.e., the amino acid sequence of the 12th to 230th amino acids in the amino acid sequence of SEQ ID NO: 1.

[0029] The term "disintegrin domain" as used herein means a domain containing an amino acid sequence having a 50% or more (preferably 93% or more) homology with the amino acid sequence of the disintegrin domain in the human ADAMTS-1 protein, i.e., the amino acid sequence of the 235th to 305th amino acids in the amino acid sequence of SEQ ID NO: 1.

[0030] The term "thrombospondin domain" as used herein means a domain containing an amino acid sequence having a 50% or more homology with at least one of the amino acid sequences of three disintegrin domains in the human ADAMTS-1 protein, that is,

(1) a domain containing an amino acid sequence having a 50% or more (preferably 99% or more) homology with the amino acid sequence of the first thrombospondin domain (hereinafter sometimes referred to as a "human TSP-1 domain") from the N-terminus in the human ADAMTS-1 protein, i.e., the amino acid sequence of the 322nd to 372nd amino acids in the amino acid sequence of SEQ ID NO: 1;

(2) a domain containing an amino acid sequence having a 50% or more (preferably 88% or more) homology with the amino acid sequence of the second thrombospondin domain (hereinafter sometimes referred to as a "human TSP-2 domain") from the N-terminus in the human ADAMTS-1 protein, i.e., the amino acid sequence of the 618th to 664th amino acids in the amino acid sequence of SEQ ID NO: 1; or

(3) a domain containing an amino acid sequence having a 50% or more (preferably 88% or more) homology with the amino acid sequence of the third thrombospondin domain (hereinafter sometimes referred to as a "human TSP-3 domain") from the N-terminus in the human ADAMTS-1 protein, i.e., the amino acid sequence of the 672nd to 727th amino acids in the amino acid sequence of SEQ ID NO: 1.

[0031] In the ADAMTS protein of the present invention, the number of each of the matrix metalloproteinase domain, the disintegrin domain, and the thrombospondin domain, and the sequential order thereof, are not particularly limited, so long as at least one matrix metalloproteinase domain, at least one disintegrin domain, and at least one thrombospondin domain are contained at the same time in the ADAMTS protein. A preferred ADAMTS protein contains a matrix metalloproteinase domain, a disintegrin domain and three thrombospondin domains. Further, the sequential order of the domains from the N-terminus to the C-terminus preferably starts from the matrix metalloproteinase domain, followed by the disintegrin domain, and then the thrombospondin domain. When three thrombospondin domains are contained, the sequential order of the domains from the N-terminus to the C-terminus preferably starts from the matrix metalloproteinase domain, followed by the disintegrin domain, and then the first TSP domain, the second TSP domain and the third TSP domain.

[0032] In the ADAMTS protein of the present invention, it is preferable that

(1) the matrix metalloproteinase domain has a 95% or more homology in the amino acid sequences with the matrix metalloproteinase domain in the human ADAMTS-1 protein,

(2) the disintegrin domain has a 93% or more homology in the amino acid sequences with the disintegrin domain in the human ADAMTS-1 protein, and

(3) at least one of the thrombospondin domains has a 99% or more homology in the amino acid sequence with the TSP-1 domain in the human ADAMTS-1 protein, an 88% or more homology in the amino acid sequences with the TSP-2 domain in the human ADAMTS-1 protein, or an 88% or more homology in the amino acid sequences with the TSP-3 domain in the human ADAMTS-1 protein.

[0033] In the present ADAMTS protein containing three thrombospondin domains, it is preferable that

(3-1) the first thrombospondin domain from the N-terminus has a 99% or more homology in the amino acid sequences with the TSP-1 domain in the human ADAMTS-1 protein,

(3-2) the second thrombospondin domain from the N-terminus has an 88% or more homology in the amino acid sequences with the TSP-2 domain in the human ADAMTS-1 protein, and

(3-3) the third thrombospondin domain from the N-terminus has an 88% or more homology in the amino acid sequences with the TSP-3 domain in the human ADAMTS-1 protein.

[0034] The protein of the present invention may be prepared by various known processes. For example, the protein

of the present invention may be prepared using a known genetic engineering technique and the gene of the present invention. Alternatively, the protein of the present invention may be purified from a naturally occurring source, using a known protein chemical technique.

[0035] The gene of the present invention includes a gene encoding the protein containing the amino acid sequence of SEQ ID NO: 1, particularly the human ADAMTS-1 protein; a gene encoding the human ADAMTS-1 protein variation; and a gene encoding the ADAMTS protein (except the mouse ADAMTS-1 protein). The present gene may be DNA or RNA. The gene encoding the human ADAMTS-1 protein may be, for example, a gene consisting of the base sequence of SEQ ID NO: 2:

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10  ATG GAT ATC TGC AGA ATT CGG CTT AGG AAG AAG CGA TTT GTG TCC AGC
    CCC CGT TAT GTG GAA ACC ATG CTT GTG GCA GAC CAG TCG ATG GCA GAA
15  TTC CAC GGC AGT GGT CTA AAG CAT TAC CTT CTC ACG TTG TTT TCG GTG
    GCA GCC AGA TTG TAC AAA CAC CCC AGC ATT CGT AAT TCA GTT AGC CTG
    GTG GTG GTG AAG ATC TTG GTC ATC CAC GAT GAA CAG AAG GGG CCG GAA
20  GTG ACC TCC AAT GCT GCC CTC ACT CTG CGG AAC TTT TGC AAC TGG CAG
    AAG CAG CAC AAC CCA CCC AGT GAC CGG GAT GCA GAG CAC TAT GAC ACA
25  GCA ATT CTT TTC ACC AGA CAG GAC TTG TGT GGG TCC CAG ACA TGT GAT
    ACT CTT GGG ATG GCT GAT GTT GGA ACT GTG TGT GAT CCG AGC AGA AGC
30  TGC TCC GTC ATA GAA GAT GAT GGT TTA CAA GCT GCC TTC ACC ACA GCC
    CAT GAA TTA GGC CAC GTG TTT AAC ATG CCA CAT GAT GAT GCA AAG CAG
35  TGT GCC AGC CTT AAT GGT GTG AAC CAG GAT TCC CAC ATG ATG GCG TCA
    ATG CTT TCC AAC CTG GAC CAC AGC CAG CCT TGG TCT CCT TGC AGT GCC
    TAC ATG ATT ACA TCA TTT CTG GAT AAT GGT CAT GGG GAA TGT TTG ATG
40  GAC AAG CCT CAG AAT CCC ATA CAG CTC CCA GGC GAT CTC CCT GGC ACC
    TTG TAC GAT GCC AAC CGG CAG TGC CAG TTT ACA TTT GGG GAG GAC TCC
45  AAA CAC TGC CCC GAT GCA GCC AGC ACA TGT AGC ACC TTG TGG TGT ACC
    GGC ACC TCT GGT GGG GTG CTG GTG TGT CAA ACC AAA CAC TTC CCG TGG
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EP 1 004 674 A1

CCG GAT GGC ACC AGC TGT GGA GAA GGG AAA TGG TGT ATC AAC GGC AAG
TGT GTG AAC AAA ACC GAC AGG AAG CAT TTT GAT ACG CCT TTT CAT GGA
AGC TGG GGA CCA TGG GGA CCG TGG GGA GAC TGT TCG AGA ACG TGC GGT
GGA GGA GTC CAG TAC ACG ATG AGG GAA TGT GAC AAC CCA GTC CCA AAG
AAT GGA GGG AAG TAC TGT GAA GGC AAA CGA GTG CGC TAC AGA TCC TGT
AAC CTT GAG GAC TGT CCA GAC AAT AAT GGA AAA ACC TTT AGA GAG GAA
CAA TGT GAA GCA CAC AAC GAG TTT TCA AAA GCT TCC TTT GGG AGT GGG
CCT GCG GTG GAA TGG ATT CCC AAG TAC GCT GGC GTC TCA CCA AAG GAC
AGG TGC AAG CTC ATC TGC CAA GCC AAA GGC ATT GGC TAC TTC TTC GTT
TTG CAG CCC AAG GTT GTT GAT GGT ACT CCA TGT AGC CCA GAT TCC ACC
TCT GTC TGT GTG CAA GGA CAG TGT GTA AAA GCT GGT TGT GAT CGC ATC
ATA GAC TCC AAA AAG AAG TTT GAT AAA TGT GGT GTT TGC GGG GGA AAT
GGA TCT ACT TGT AAA AAA ATA TCA GGA TCA GTT ACT AGT GCA AAA CCT
GGA TAT CAT GAT ATC GTC ACA ATT CCA ACT GGA GCC ACC AAC ATC GAA
GTG AAA CAG CGG AAC CAG AGG GGA TCC AGG AAC AAT GGC AGC TTT CTT
GCC ATC AAA GCT GCT GAT GGC ACA TAT ATT CTT AAT GGT GAC TAC ACT
TTG TCC ACC TTA GAG CAA GAC ATT ATG TAC AAA GGT GTT GTC TTG AGG
TAC AGC GGC TCC TCT GCG GCA TTG GAA AGA ATT CGC AGC TTT AGC CCT
CTC AAA GAG CCC TTG ACC ATC CAG GTT CTT ACT GTG GGC AAT GCC CTT
CGA CCT AAA ATT AAA TAC ACC TAC TTC GTA AAG AAG AAG AAG GAA TCT
TTC AAT GCT ATC CCC ACT TTT TCA GCA TGG GTC ATT GAA GAG TGG GGC
GAA TGT TCT AAG TCA TGT GAA TTG GGT TGG CAG AGA AGA CTG GTA GAA
TGC CGA GAC ATT AAT GGA CAG CCT GCT TCC GAG TGT GCA AAG GAA GTG
AAG CCA GCC AGC ACC AGA CCT TGT GCA GAC CAT CCC TGC CCC CAG TGG
CAG CTG GGG GAG TGG TCA TCA TGT TCT AAG ACC TGT GGG AAG GGT TAC
AAA AAA AGA AGC TTG AAG TGT CTG TCC CAT GAT GGA GCG GTG TTA TCT

CAT GAG AGC TGT GAT CCT TTA AAG AAA CCT AAA CAT TTC ATA GAC TTT

TGC ACA CTG ACA CAG TGC AGT TAA

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[0036] The gene of the present invention, such as the gene consisting of the base sequence of SEQ ID NO: 2, may be obtained, for example, by the following method, which was used by the present inventors when the present gene was obtained for the first time.

[0037] That is, various suitable primers for a PCR are prepared on the basis of the base sequence of the mouse ADAMTS-1 gene. DNA fragments may be obtained by carrying out a PCR under a condition milder than that of an ordinary PCR, i.e., at an annealing temperature lower than a usual annealing temperature, using a human kidney cDNA library as templates. Base sequences of the resulting DNA fragments are determined, and compared with the base sequence of the mouse ADAMTS-1 gene, to thereby identify the resulting DNA fragments as the desired genes. Depending on the primers used in the PCR, a full-length human ADAMTS-1 gene or a partial base sequence of the human ADAMTS-1 gene may be obtained. When the partial base sequence is obtained, the remaining base sequence of the gene may be obtained by a RACE (Rapid amplification of cDNA ends) method [Proc Natl. Acad. Sci. USA, 85, 8998-9002 (1988)], and partial base sequences may be ligated by genetic-engineering to obtain the full-length base sequence.

[0038] When the present inventors designed the base sequences of the primers used to obtain the gene in the above method for the first time, the base sequence of the human ADAMTS-1 gene was not known. Therefore, it was almost impossible to select base sequences having a complete homology between the mouse ADAMTS-1 gene and the human ADAMTS-1 gene.

[0039] The present inventors used primers designed on the basis of the base sequence of the mouse ADAMTS-1 gene to carry out a PCR at a usual temperature, but a desired DNA fragment could not be obtained. However, the present inventors used the same primers and carried out a PCR under a condition milder than that of an ordinary PCR, i.e., an annealing temperature was set lower than a usual annealing temperature, whereby the desired DNA fragment was able to be obtained. The comparison of the base sequence of the resulting human ADAMTS-1 gene with the base sequences of the primers used revealed an insufficient homology.

[0040] At present, the base sequence of the human ADAMTS-1 gene has been determined according to the present invention. Therefore, the base sequence of the human ADAMTS-1 gene may be used to design primers for a PCR or probes for plaque hybridization. Such primers or probes may be used to obtain the gene of the present invention by a known method to obtain a gene, such as a PCR under ordinary conditions or plaque hybridization, instead of the method used by the present inventors to obtain the present gene for the first time.

[0041] The present inventors attempted to obtain an unknown human ADAMTS-1 gene from the human kidney cDNA library by plaque hybridization, using probes designed on the basis of the base sequence of the known mouse ADAMTS-1 gene, but a desired gene was not obtained. One of the reasons of this failure was an insufficient homology of the probes used. Further, the present inventors have carried out northern hybridization to analyze the mRNA of the human ADAMTS-1 protein, and confirmed that the failure must also have occurred because mRNA is expressed in a very small amount, and thus a very small number of the human ADAMTS-1 genes are copied in a cDNA library.

[0042] The gene of the present invention may be obtained by plaque hybridization, using probes designed on the basis of the base sequence of the human ADAMTS-1 gene.

[0043] The resulting gene of the present invention may be expressed in, for example, a eucaryotic or procaryotic host to produce the protein of the present invention.

[0044] If a DNA fragment containing a desired gene is directly introduced into a host cell, the fragment is not reproduced. However, an extrachromosomal gene reproducible in a cell, such as a plasmid, may be used as a vector to prepare an expression plasmid. A vector which may be used preferably contains genetic information necessary for replication in a host cell, can be independently replicated, is easily isolated and purified from a host cell, and contains a detectable marker.

[0045] An expression vector containing the DNA of the present invention may be constructed in accordance with a host cell from various commercially available vectors. A method for introducing the DNA into the vector is well known.

[0046] As a procaryotic host, there may be mentioned, for example, E. coli strains, such as XL1-Blue, HB101, JM109, DH5 α , AG-1, K12 strain 294 (ATCC 31446), B, χ 1776 (ATCC 31537), C600, or W3110 (F⁻, λ ⁻, prototrophic; ATCC 27375). Further, Bacillus strains, such as Bacillus subtilis, enteric bacteria, such as Salmonella typhimurium or Serratia marcescens, or Pseudomonas strains may be used.

[0047] When the procaryotic host is used, an expression plasmid which may be used as a vector contains a pro-

moter, an SD base sequence, and a base sequence necessary for initiating a protein synthesis, i.e., ATG, upstream of the gene of the present invention so as to express the gene. As a vector for *E. coli* strains, pUC19, pBR322, or pBR327 are generally and widely used.

[0048] As a promoter, for example, triptophan promoter, P_L promoter, lac promoter, tac promoter, trc promoter, lpp promoter, or β -lactamase promoter may be used. Examples of the marker gene are an ampicillin resistance gene or tetracycline resistance gene.

[0049] As a eucaryotic host, a yeast is generally and widely used. Of the yeasts, a *Saccharomyces* yeast can be advantageously used. As an expression vector for the eucaryotic host such as a yeast, for example, YRp7 may be used

[0050] As a promoter of the expression vector for a yeast expression, for example, alcohol dehydrogenase (ADH), GAL10, 3-phosphoglycerate kinase, enolase, glyceraldehyde-3-phosphate dehydrogenase, or hexokinase may be used. An example of a marker gene is a *trp1* gene.

[0051] As a replication origin, a stop codon, or other DNA sequences used to control a transcription or translation in a yeast cell, usual known DNA sequences suitable to the yeast cell may be used.

[0052] As a culture cell host of a higher animal, there may be mentioned, for example, a rhesus renal cell, a mosquito larva cell, an African Green Monkey kidney cell (COS-7 or COS-1), a murine fetal fibroblast, a Chinese hamster ovary cell or a dihydrofolate reductase-defective strain thereof, a human cervical epitheliocyte, a human fetal kidney cell, a moth ovary cell, a human myeloma cell, or a murine fibroblast cell.

[0053] The vector generally contains functional sequences to express the DNA of the present invention in a host cell, for example, a replication origin, a promoter, which should be upstream of the DNA of the present invention, a ribosome binding site, a polyadenylated site, and/or a transcription termination sequence. A preferable promoter is, for example, an adenovirus 2 main late promoter, SV40 early promoter, SV40 late promoter, or a promoter from cytomegalovirus, Rous sarcoma virus, or an eucaryote gene, such as estrogen inducible chick egg albumin gene, interferon gene, glucocorticoid inducible threonine aminotransferase gene, thymidine kinase gene, main early and late adenovirus gene, phosphoglycerate kinase gene, or α factor gene.

[0054] A replication origin from adenovirus, SV40, bovine papilloma virus (BPV), vesicular stomatitis virus (VSV), or a derivative vector thereof may be used as the replication origin. In these cases, for example, a neomycin resistance gene, a methotrexate resistant dihydrofolate reductase (DHR) gene, or a blasticidin S resistance gene may be used as the marker gene.

[0055] As an insect cell host, for example, BmN4 cell, Sf9 cell, Sf21 cell, or an ovary cell of *Trichoplusia* may be used. Further, a larval silkworm individual may be used as a host. A gene transfer to the insect cell can be carried out by co-infecting the insect cell with a virus DNA and a transfer vector containing a desired gene to be incorporated. As the virus DNA, for example, a *Bombyx mori* nuclear polyhedrosis virus, or *Autographica californica* multiple nuclear polyhedrosis virus may be used. As the transfer vector containing the desired gene to be inserted, for example, a polyhedrin promoter or p10 promoter vector may be used. The desired gene can be inserted downstream of the promoters. The transfer vector can be replicated in *E. coli*, but cannot be replicated in an insect cell. Therefore, it is preferable to replicate many vectors in *E. coli*, and then express them in the insect cell. According to this process, a larger amount of expressed substances can be recovered in comparison with an animal cell.

[0056] The resulting expression plasmid may be transfected into an appropriate host cell, for example, a microorganism cell, such as *E. coli* yeast, or an animal cell, to produce the transformant of the present invention. The method for transfecting the DNA may be, for example, a method of utilizing a competent cell treated with calcium chloride, a protoplast method, a calcium phosphate transfection method, or an electroporation method.

[0057] The pharmaceutical composition of the present invention comprises (1) the protein containing the amino acid sequence of SEQ ID NO: 1, particularly the human ADAMTS-1 protein, (2) the human ADAMTS-1 protein variation, or (3) the ADAMTS protein, as an active ingredient. In the pharmaceutical composition of the present invention, the active ingredient may be the mouse ADAMTS-1 protein. The proteins which may be used as the active ingredient of the pharmaceutical composition in the present invention have activities to influence hematopoietic functions, for example, activities to decrease the number of leukocytes and platelets, and at the same time, increase the number of erythrocytes, when administered into a blood vessel.

[0058] It is possible to orally or parenterally administer the pharmaceutical composition according to the present invention, i.e., the protein containing the amino acid sequence of SEQ ID NO: 1, particularly the human ADAMTS-1 protein, the human ADAMTS-1 protein variation, or the ADAMTS protein, alone or preferably together with a pharmaceutically or veterinarily acceptable ordinary carrier, to an animal, preferably a mammal, particularly humans. The formulation is not particularly limited to, but may be, for example, oral medicines, such as powders, fine subitlaes, granules, tablets, capsules, suspensions, emulsions, syrups, extracts or pills, or parenteral medicines, such as injections, liquids for external use, ointments, suppositories, creams for topical application, or eye lotions.

[0059] The oral medicines may be prepared by an ordinary method using, for example, fillers, binders, disintegrating agents, surfactants, lubricants, flowability-enhancers, diluting agents, preservatives, coloring agents, perfumes, tasting agents, stabilizers, humectants, antiseptics, antioxidants, such as gelatin, sodium alginate, starch, corn starch,

saccharose, lactose, glucose, mannitol, carboxymethylcellulose, dextrin, polyvinyl pyrrolidone, crystalline cellulose, soybean lecithin, sucrose, fatty acid esters (such as glycerin fatty acid ester, sucrose fatty acid ester, sorbitan fatty acid ester, or propyleneglycol fatty acid ester), talc, magnesium stearate, polyethylene glycol, magnesium silicate, silicic anhydride, or synthetic aluminum silicate.

5 [0060] For the parenteral administration, for example, an injection such as a subcutaneous or intravenous injection, or the per rectum administration may be used. Of the parenteral formulations, an injection is preferably used.

[0061] Then the injections are prepared, for example, water-soluble solvents, such as physiological saline or Ringer's solution, water-insoluble solvents, such as plant oil or fatty acid ester, agents for rendering isotonic, such as glucose or sodium chloride, solubilizing agents, stabilizing agents, antiseptics, suspending agents, or emulsifying agents may be optionally used, in addition to the protein containing the amino acid sequence of SEQ ID NO: 1, particularly the human ADAMTS-1 protein, the human ADAMTS-1 protein variation, or the ADAMTS protein.

10 [0062] The pharmaceutical composition may be administered in the form of a sustained release preparation using sustained release polymers. For example, the pharmaceutical composition of the present invention may be incorporated to a pellet made of ethylenevinyl acetate polymers, and the pellet may be surgically implanted in a tissue to be treated.

15 [0063] The pharmaceutical composition of the present invention may contain the protein containing the amino acid sequence of SEQ ID NO: 1, particularly the human ADAMTS-1 protein, the human ADAMTS-1 protein variation, or the ADAMTS protein in an amount, but not particularly limited to, of 0.0001 to 99% by weight, preferably 0.01 to 80% by weight, more preferably 0.01 to 50% by weight.

20 [0064] When the pharmaceutical composition of the present invention is utilized, the dose is not particularly limited, but varies with the kind of disease, the age, sex, body weight, or symptoms of the subject, a method of administration, or the like. However, the protein containing the amino acid sequence of SEQ ID NO: 1, particularly the human ADAMTS-1 protein, the human ADAMTS-1 protein variation, or the ADAMTS protein may be orally or parenterally administered at a dosage of about 0.0001 $\mu\text{g/kg}$ to 10,000 $\mu\text{g/kg}$, preferably 0.001 $\mu\text{g/kg}$ to 1,000 $\mu\text{g/kg}$, more preferably 0.01 $\mu\text{g/kg}$ to 100 $\mu\text{g/kg}$ a day for an adult, usually once or divided into up to four dosages.

25 [0065] The pharmaceutical composition of the present invention may be used not only for the pharmaceutical application but also for various applications. That is, the protein containing the amino acid sequence of SEQ ID NO: 1, particularly the human ADAMTS-1 protein, the human ADAMTS-1 protein variation, or the ADAMTS protein may be administered in the form of functional food or health food, together with a conventional food additive, or directly added to food as a food additive.

30 [0066] The pharmaceutical composition of the present invention contains the protein containing the amino acid sequence of SEQ ID NO: 1, particularly the human ADAMTS-1 protein, the human ADAMTS-1 protein variation, or the ADAMTS protein, and thus is useful as, for example, an agent for reducing leukocytes, an agent for reducing platelets, or an agent for increasing erythrocytes.

35 [0067] It is generally known that, when inflammation occurs, leukocytes are activated in blood, move to an inflamed site, evolve and/or cause pathosis. Therefore, it is believed that the human ADAMTS-1 protein of the present invention would be effective in the treatment of various inflammatory diseases, such as rheumatic arthritis, psoriasis, asthma, hepatitis, Kawasaki disease, gout, adult respiratory distress syndrome (ARDS), Crohn's disease, ulcerative colitis, sepsis, or nephritis. Further, the human ADAMTS-1 protein of the present invention exhibits a function to decrease the number of leukocytes and platelets, and thus would be effective in a treatment of true hypervolemia. The human ADAMTS-1 protein of the present invention exhibits a function to decrease the number of platelets. Therefore, it is believed that the human ADAMTS-1 protein of the present invention would exhibit an anti-thrombotic action, and would be effective in the treatment of cardiac infarction, cerebral infarction, or multi-organ failure. The human ADAMTS-1 protein of the present invention exhibits a function to significantly increase the number of erythrocytes, and would be effective in a treatment of anemia, as erythropoietin.

45 [0068] When lipopolysaccharide (LPS), an immunologically stimulating substance, is administered to a mouse (for example, a 10 $\mu\text{g/mouse}$), an expression of the mouse ADAMTS-1 gene is superinduced in a heart and a kidney [J. Biol. Chem., 272, 556-562 (1997)]. Therefore, the mouse ADAMTS-1 protein would possibly exhibit a protective function for a heart, and a kidney, upon a lethally acute inflammation such as an endotoxin shock.

50 [0069] Thrombospondin (TSP) is known as a factor for inhibiting vascularization, i.e., specifically inhibiting a growth of endothelial cells [J. Cell. Biol., 111, 765-772 (1990)]. Further, it was reported that the proliferation and metastasis of cancer cells can be inhibited by the induction of TSP in cancer cells [J. Cell. Biol., 111, 765-772 (1990)]. Therefore, the human ADAMTS-1 protein would probably show a function for inhibiting a cancer or metastasis. Further, a recent report had stated that TSP or disintegrin is involved in a bone formation [Biochem. Biophys. Res. Commun., 213, 1017-1025 (1995)]. Therefore, the human ADAMTS-1 protein could be applicable to the treatment of a metabolic bone disease, such as osteoporosis.

55 [0070] The immunologically reactive substance of the present invention specifically reacts the protein containing the amino acid sequence of SEQ ID NO: 1, particularly the human ADAMTS-1 protein, the human ADAMTS-1 protein

variation, or the ADAMTS protein. The immunologically reactive substance of the present invention includes, for example, an antibody (a monoclonal antibody or a polyclonal antibody), fragments of the antibody, such as, Fab, Fab', F(ab')₂, or Fv, and an antiserum. The immunologically reactive substance of the present invention specifically reacts the human ADAMTS-1 protein, and therefore, the immunologically reactive substance of the present invention specifically reacts the human ADAMTS-1 protein, and therefore, is useful for analyzing the human ADAMTS-1 protein by immunological ways.

[0071] The monoclonal antibody of the present invention may be prepared by a known method, for example, the following method.

[0072] A physiological salt solution containing an antigen is mixed with an equal volume of complete Freund's adjuvant or incomplete adjuvant, or an equivalent thereof, such as Hunter's TiterMax™ (Funakoshi; Cat. No. YT001-00, Tokyo, Japan), until emulsified. The resulting emulsion is administered subcutaneously, intraperitoneally, intravenously, intramuscularly, or intradermally to a mammal, for example, a mouse, rat, rabbit, or hamster, more particularly, a mouse, such as a BALB/c mouse, selected in view of a congeniality to a conventional myeloma cell (a first immunization). Then, the same procedure is repeated at intervals of two to four weeks for several immunizations, and final immunization is carried out using only the antigen solution. The spleens are removed aseptically several days after the final immunization, and spleen cells are prepared.

[0073] The resulting spleen cells are used for a cell fusion. The other parent cells used for the cell fusion, that is, the myeloma cells, may be known cell lines, such as, P3X63-Ag8(X63) [Nature, 256, 495-497 (1975)], P3X63-Ag8U1 (P3U1) [Current Topics in Microbiology and Immunology, 81, 1-7 (1978)], or P3X63Ag8.653 (ATCC deposition No. CRL-1580).

[0074] The cell fusion may be carried out by usual methods, for example, the method of Milstein et. al. [Methods in Enzymology, 73, 3-47 (1981)]. The resulting hybridomas are administered to mammals (for example, mice), and desired monoclonal antibodies are separated and purified from ascites of the mammals. The separation and purification method used may be a known method, such as a dialysis ion exchange chromatography using an ammonium sulfate; an affinity column chromatography using a protein A or protein G binding polysaccharides carrier or an anti-mouse immunoglobulin antibody binding polysaccharides carrier; dialysis, or lyophilization.

[0075] The polyclonal antibody of the present invention may be prepared by a known method, as indicated below. That is, a physiological salt solution containing an antigen is mixed with an equal volume of complete Freund's adjuvant or incomplete adjuvant, or an equivalent thereof, such as Hunter's TiterMax™ (Funakoshi; Cat. No. YT001-00, Tokyo, Japan), until emulsified. The resulting emulsion is administered subcutaneously, intraperitoneally, or intramuscularly to a mammal, for example, a rabbit, or goat (a first immunization). Then, the same procedure is repeated at intervals of two to four weeks for several immunizations. One or two weeks after a final immunization, blood is taken from a carotid artery or a heart of the mammal, and salted-out with ammonium sulfate to prepare a serum.

[0076] The antibody fragment of the present invention may be prepared, for example, by digesting the polyclonal antibody or monoclonal antibody of the present invention with a known protease by a conventional method, and then isolating and purifying by a conventional method.

[0077] Production of the human ADAMTS-1 protein is facilitated by an immunologically stimulating substance, such as LPS, and therefore, the human ADAMTS-1 protein may be used as a diagnostic marker of an immunological state in a method for extracorporeally detecting the immunological state. More particularly, the extracorporeally detecting method of the present invention may be applied to a sample taken from a subject to be examined, to thereby detect an immunological state of an immune function of the subject, when the immune function is affected by various diseases, such as inflammation, cancer, cachexia, such as cancer cachexia or infectious disease-related cachexia, infectious disease, or leukemia. If the immune function of the subject is normal, an immunological state corresponding to the immune function can be detected.

[0078] The sample which may be used in the present invention is not particularly limited, so long as it has a possibility of including the human ADAMTS-1 protein. The sample may be a biological sample taken from a human, particularly a patient, for example, a humor, such as a tissue (e.g., cells) or an extract therefrom, blood, such as serum, and plasma, urine, or cerebrospinal fluid. A sample used in a conventional clinical examination may be used in the present invention without limitation.

[0079] In the analysis step of the human ADAMTS-1 protein in the sample, the sample is first brought into contact with the substance immunologically reactive to the human ADAMTS-1 protein. If the sample does not contain the human ADAMTS-1 protein, a reaction with the immunologically reactive substance does not occur. If the sample contains the human ADAMTS-1 protein, the immunologically reactive substance binds the human ADAMTS-1 protein, and a complex of the immunologically reactive substance and the human ADAMTS-1 protein is formed in an amount correlated with that of the human ADAMTS-1 protein present in the sample. The complex may be easily detected by a known method, and therefore, an existence of the human ADAMTS-1 protein in the sample can be detected by detecting the existence of the complex, or an amount of the human ADAMTS-1 protein in the sample can be measured by measuring the amount of the complex. The human ADAMTS-1 protein in a tissue or a cell may be measured, using a tissue section

sample or a cell sample in a fluorescent antibody technique or an enzyme antibody technique.

[0080] The immunologically reactive substance capable of immunologically reacting the human ADAMTS-1 protein includes an anti-human ADAMTS-1 protein antiserum, an anti-human ADAMTS-1 protein polyclonal antibody, of an anti-human ADAMTS-1 protein monoclonal antibody, or a fragment thereof. The immunologically reactive substance may be used singly or in combination thereof. The fragment includes, for example, Fab, Fab', F(ab')₂, or Fv.

[0081] In the method for immunologically analyzing the human ADAMTS-1 protein according to the present invention, the sample is brought into contact with the immunologically reactive substance capable of immunologically reacting the human ADAMTS-1 protein, and a complex of the human ADAMTS-1 protein and the immunologically reactive substance is formed. Then, the human ADAMTS-1 protein bound to the antibody is detected and the amount thereof is measured by an immunochemical method, to thereby find a level of the human ADAMTS-1 protein in the sample.

[0082] The immunochemical method principally may be, for example, any conventional immunoassay, for example, EIA, ELISA, RIA or the like. The immunochemical methods are generally classified as follows:

(1) Competitive assay:

[0083] A sample containing an unknown amount of antigens and a given amount of labeled antigens is competitively reacted with a given amount of antibodies, and then an activity of the labeled antigens bound to the antibodies or an activity of the labeled antigens not bound to the antibodies is measured.

(2) Sandwich assay:

[0084] An excess amount of antibodies immobilized on carriers is added and reacted to a sample containing an unknown amount of antigens (a first reaction). Then, a given excess amount of labeled antibodies is added and reacted therewith (a second reaction). An activity of the labeled antibodies on the carriers is measured. Alternatively, an activity of the labeled antibodies which are not on the carriers is measured. The first reaction and the second reaction may be carried out at the same time, or sequentially.

[0085] When a labeling agent is a radioactive isotope, a well counter or a scintillation counter may be used for measurement. When the labeling agent is an enzyme, an enzymatic activity can be measured by colorimetry or fluorimetry, after adding a substrate and allowing to stand. When the labeling agent is a fluorescent substance or a luminescent substance, a known method therefor may be used, respectively.

[0086] In addition to the above methods, recently a western blotting method has been used wherein electrophoresed proteins are transferred onto a filter such as a nitrocellulose membrane, and a target protein is detected with an antibody. The western blotting method may also be used in the detection of the human ADAMTS-1 protein in the present invention.

[0087] The antibody used in the above methods can be labeled with an appropriate marker. Examples are a radioactive isotope, an enzyme, a fluorescent substance, or a luminescent substance, by a known method of labeling antibodies.

[0088] The radioactive isotope may be, for example, ¹²⁵I, ¹³¹I, ³H, ¹⁴C, or ³⁵S.

[0089] Preferably, the enzyme used is stable and has a large specific activity. Examples of the enzyme are a glycosidase (such as, β -galactosidase, β -glucosidase, β -glucuronidase, β -fructosidase, α -galactosidase, α -glucosidase, or α -mannosidase), an amylase (such as, α -amylase, β -amylase, isoamylase, glucoamylase, or taka-amylase), a cellulase, or a carbohydrase such as lysozyme; a urease, or an amidase such as asparaginase; a choline esterase, such as acetylcholinesterase, a phosphatase, such as alkaline phosphatase, a sulfatase, an esterase such as lipase; a nuclease such as deoxyribonuclease or ribonuclease; an iron porphyrin enzyme, such as a catalase, peroxidase or cytochrome oxidase; a copper enzyme, such as a tyrosinase or ascorbate oxidase; dehydrogenase, such as an alcohol dehydrogenase, malate dehydrogenase, lactate dehydrogenase, or isocitrate dehydrogenase.

[0090] The fluorescent substance may be, for example, fluorescamine, or a fluorescence isothiocyanate, and the luminescent substance may be, for example, luminol, a luminol derivative, luciferin or lucigenin. A signal from the above label may be detected by known methods.

[0091] The labeling agent can be bound to antibodies by any conventional method, such as a chloramin T method [Nature, 194, 495-496, (1962)], a periodic acid method [Journal of Histochemistry and Cytochemistry, 22, 1084-1091, (1974)], or a maleimide method [Journal of Biochemistry, 79, 233-236, (1976)].

[0092] An EIA method as one of the above measurement methods will be mentioned hereinafter. A sample is added to the first anti-human ADAMTS-1 protein antibodies immobilized on a carrier (such as an assay plate), and the anti-human ADAMTS-1 protein antibodies are bound to the human ADAMTS-1 proteins to form complexes. To the complexes, the second anti-human ADAMTS-1 protein antibodies labeled with enzyme (such as peroxidase) are added to react with the complexes to form "first antibody/human ADAMTS-1 protein/second antibody" complexes. To the resulting "first antibody/human ADAMTS-1 protein/second antibody" complexes, a substrate for the enzyme label (such as

peroxidase) is added, and an absorbance or fluorescent strength of products of the enzymatic reaction is measured, whereby enzymatic activities of the enzyme labels attached to the "first antibody/human ADAMTS-1 protein/second antibody" complexes are measured. A series of the above procedures is carried out in advance for a standard solution containing a known amount of the human ADAMTS-1 protein, and a standard curve based on the relationship between the human ADAMTS-1 protein and the absorbance or fluorescent strength is prepared. A comparison is made between the standard curve and absorbance or fluorescent strength for a sample containing an unknown amount of the human ADAMTS-1 proteins, and the amount of the human ADAMTS-1 proteins in the sample can be measured.

[0093] Another EIA method will be mentioned hereinafter. A sample is brought into contact with a carrier (such as an assay plate) to immobilize the human ADAMTS-1 proteins in the sample onto the carrier. Then, the anti-human ADAMTS-1 protein antibodies (first antibodies) are added thereto to form complexes of the human ADAMTS-1 protein and the first antibody. To the complexes are added anti-first antibody antibodies (second antibodies) labeled with enzyme (such as peroxidase), to react with the complexes to form "human ADAMTS-1 protein/first antibody/second antibody" complexes. To the resulting "human ADAMTS-1 protein/first antibody/second antibody" complexes is added a substrate for the enzyme label (such as peroxidase), and the absorbance or fluorescent strength of products of the enzymatic reaction is measured, whereby enzymatic activities of the enzyme labels attached to the "human ADAMTS-1 protein/first antibody/second antibody" complexes are measured. A series of the above procedures is carried out in advance for a standard solution containing a known amount of the human ADAMTS-1 protein, and a standard curve based on the relationship between the human ADAMTS-1 protein and the absorbance or fluorescent strength is prepared. A comparison is made between the standard curve and the absorbance or fluorescent strength for a sample containing an unknown amount of the human ADAMTS-1 proteins, and the amount of the human ADAMTS-1 proteins in the sample can be measured.

[0094] Further, an RIA method will be mentioned hereinafter. A sample is added to the first anti-human ADAMTS-1 protein antibodies immobilized on a carrier (such as a test tube), and the anti-human ADAMTS-1 protein antibodies are bound to the human ADAMTS-1 proteins to form complexes. To the complexes are added the second anti-human ADAMTS-1 protein antibodies labeled with radioactive isotope (such as ^{125}I), to react with the complexes to form "first antibody/human ADAMTS-1 protein/second antibody" complexes. A radioactivity of the resulting "first antibody/human ADAMTS-1 protein/second antibody" complexes is measured. A series of the above procedures is carried out in advance for a standard solution containing a known amount of the human ADAMTS-1 protein, and a standard curve based on the relationship between the human ADAMTS-1 protein and the radioactivity is prepared. A comparison is made between the standard curve and the radioactivity for a sample containing an unknown amount of the human ADAMTS-1 proteins, and the amount of the human ADAMTS-1 proteins in the sample can be measured.

[0095] Another RIA method will be mentioned hereinafter. A sample is brought into contact with a carrier (such as a test tube) to immobilize the human ADAMTS-1 proteins in the sample onto the carrier. Then, the anti-human ADAMTS-1 protein antibodies (first antibodies) are added thereto to form complexes of the human ADAMTS-1 protein and the first antibody. To the complexes are added anti-first antibody antibodies (second antibodies) labeled with radioactive isotope (such as ^{125}I), to react with the complexes to form "human ADAMTS-1 protein/first antibody/second antibody" complexes. A radioactivity of the resulting "human ADAMTS-1 protein/first antibody/second antibody" complexes is measured. A series of the above procedures is carried out in advance for a standard solution containing a known amount of the human ADAMTS-1 protein, and a standard curve based on the relationship between the human ADAMTS-1 protein and the radioactivity is prepared. A comparison is made between the standard curve and the radioactivity for a sample containing an unknown amount of the human ADAMTS-1 proteins, and the amount of the human ADAMTS-1 proteins in the sample can be measured.

[0096] In the method for analyzing the mRNA of the human ADAMTS-1 protein in a sample, the sample is reacted with a polynucleotide containing a base sequence complementary to that of the mRNA of the human ADAMTS-1 protein, and the resulting complex of the mRNA of the human ADAMTS-1 protein and the polynucleotide is detected, or the amount of the complex is measured to thereby analyze the mRNA of the human ADAMTS-1 protein.

[0097] The polynucleotide contains a sequence complementary or substantially complementary to that of a part of the mRNA transcribed from a selected gene (DNA), and thus forms a double strand with the mRNA transcribed from the target gene. It is believed that any polynucleotide sufficiently complementary to form a stable complex with a target mRNA can be used. The polynucleotide able to be used in the present invention may be complementary to substantially any region in a target mRNA. The polynucleotide can be used as a DNA probe for detecting an increase or a decrease of expression of the mRNA specific to the human ADAMTS-1 protein gene. That is, the polynucleotide is specifically attached to the mRNA of the target human ADAMTS-1 protein, and forms a molecular hybrid, whereby a degree of expression of the human ADAMTS-1 protein in cells can be detected.

[0098] The polynucleotide able to be used in the present invention may be prepared by appropriately selecting a base sequence complementary to a specific base sequence of the mRNA of the target human ADAMTS-1 protein, and using a known DNA synthesizer, a known PCR apparatus, a gene cloning or the like. Various length polynucleotides may be used, but the polynucleotide preferably has 10 or more bases, more preferably 17 or more bases.

[0099] The polynucleotide may be a non-modified polynucleotide or a polynucleotide analogue. An appropriate analogue may be, for example, an ethyl or methyl phosphate analogue, or a phosphorothioated polydeoxynucleotide [Nucleic Acids Res., 14, 9081-9093, (1986); J. Am. Chem. Soc., 106, 6077-6079, (1984)], with recent improvement in the production of polynucleotide analogue, for example, a 2'-O-methylribonucleotide [Nucleic Acids Res., 15, 6131-6148, (1987)], or a conjugated RNA-DNA analogue, i.e., chimera polynucleotide [FEBS Lett., 215, 327-330, (1987)], may be used.

[0100] The selected polynucleotide may be of any kind, for example, may have an electrical charge or no electrical charge. The polynucleotide may be labeled with a known labeling agent, such as a radioactive isotope, or a fluorescent substance by a conventional method, so as to carry out the above experiment in vitro or in vivo. The radioactive isotope may be, for example, ^{125}I , ^{131}I , ^3H , ^{14}C , ^{32}P , or ^{35}S . Of these radioactive isotopes, it is preferable to label the polynucleotide with ^{32}P by a random primer method [Anal. Biochem., 132, 6-13, (1983)]. Further, a fluorescent coloring agent forming a derivative may be used as a labeling agent, as this enables an easy handling with a low risk factor. As the fluorescent coloring agent, any coloring agents capable of binding the polynucleotide may be used. For example, fluorescein, rhodamin, Texas red, 4-fluoro-7-nitrobenzofurazane (NBD), coumarin, fluorescamine, succinyl fluorescein, or dansyl may be preferably used.

[0101] An amount of an mRNA of the human ADAMTS-1 protein may be measured by a northern blotting method, using cDNA of the human ADAMTS-1 protein as follows: an mRNA is extracted and isolated from any somatic cell or tissue, then the isolated mRNA is electrophoresed on an agarose gel and transferred onto a nitro cellulose or nylon membrane, and then reacted with a labeled human ADAMTS-1 protein cDNA probe to measure an amount of the mRNA of the human ADAMTS-1 protein. The human ADAMTS-1 protein cDNA probe used is a DNA complementary to the human ADAMTS-1 protein mRNA, and has preferably 17 or more bases.

[0102] The agent for analyzing an immunological state according to the present invention contains, as a main ingredient, the immunologically reactive substance capable of immunologically reacting the human ADAMTS-1 protein. The immunologically reactive substance capable of immunologically reacting the human ADAMTS-1 protein may be, for example, an anti-human ADAMTS-1 protein antiserum, an anti-human ADAMTS-1 protein polyclonal antibody, or an anti-human ADAMTS-1 protein monoclonal antibody, or a fragment of the antibodies.

[0103] The agent for analyzing an immunological state according to the present invention may contain, as a main ingredient, the polynucleotide containing the base sequence complementary to that of an mRNA of the human ADAMTS-1 protein, instead of the immunologically reactive substance.

[0104] The human ADAMTS-1 protein per se or an mRNA of the human ADAMTS-1 protein in a sample can be analyzed according to the above methods using the agent for analyzing an immunological state according to the present invention, and the immunological state of a subject to be examined, wherein the immune function is affected by various diseases, can be judged from the result.

EXAMPLES

[0105] The present invention now will be further illustrated by, but is by no means limited to, the following Examples.

Example 1: Isolation of the human ADAMTS-1 cDNA and determination of the base sequence thereof

[0106] As primers for a PCR method, a DNA [hereinafter referred to as a "forward primer (1)"] having the base sequence (i.e., the base sequence of SEQ ID NO: 4: AGAACCTGTG GTGGTGGAGT TCAATACACA) corresponding to an amino acid sequence (i.e., the amino acid sequence of SEQ ID NO: 3: Arg Thr Cys Gly Gly Val Gln Tyr Thr) contained in the first thrombospondin (TSP) domain from the N-terminus among three TSP domains of the mouse ADAMTS-1 protein [J. Biol. Chem., 272, 556-562 (1997)], and a DNA [hereinafter referred to as a "back primer (1)"] having the base sequence (i.e., the base sequence of SEQ ID NO: 5: CCTCTTAACT GCACTGTGTC AGTGTGCAAA AG) complementary to the base sequence encoding amino acids in the C-terminus of the mouse ADAMTS-1 protein and the base sequence in the vicinal regions (i.e., the regions upstream and downstream of the C-terminus) were chemically synthesized.

[0107] To 99 μl of a solution containing 0.5 μM forward primer (1), 0.5 μM back primer (1), 0.5 units of Taq polymerase (Ex Taq polymerase; Takarashuzo, Kyoto, Japan), and 40 μM 4dNTP in a PCR buffer [10 mM Tris-HCl (pH 8.3), 50mM KCl] (Ex Taq buffer; Takarashuzo, Kyoto, Japan), 1 μl of a human kidney cDNA library (Marathon-Ready cDNA; Clontech Lab. Inc., Palo Alto, CA, USA) was added as a template DNA. A PCR method was performed at an annealing temperature lower than that used in a standard PCR method. That is, the PCR reaction was carried out by repeating a cycle composed of denaturation at 94°C for 30 seconds, annealing at 50°C for 30 seconds, and DNA synthesis at 72°C for 2 minutes, 40 times, i.e., 40 cycles.

[0108] A sample (5 μl) was taken from the resulting reaction mixture, and electrophoresed on 1% agarose gel. As shown in Fig. 1, a single DNA band of 1.2 Kb was observed. The rest of the reaction mixture was electrophoresed, and

the DNA fragment of 1.2 Kb (hereinafter sometimes referred to as a "Flag. 1 DNA fragment") was recovered from a low-melting-point agarose gel. Then, the Flag. 1 DNA fragment was cloned in a pCR™ 2.1 vector (Invitrogen Corp., San Diego, CA, USA).

[0109] A part (303 bp) of the base sequence of the cloned Flag. 1 DNA fragment was determined by an automatic DNA sequencer (DSQ1000; Shimadzu Corp., Kyoto, Japan). A homology search between the partial base sequence of the cloned Flag. 1 DNA fragment and the base sequence of the mouse ADAMTS-1 was conducted to find that a homology in the base sequences was 77.4%. The partial base sequence of the Flag. 1 DNA fragment and a partial base sequence of the mouse ADAMTS-1 gene having a homology therewith are shown in Fig. 2. The symbol ":" in Fig. 2 means that a base in the Flag. 1 DNA fragment is identical to a corresponding base in the mouse ADAMTS-1 gene.

[0110] Further, a dot hybridization (Biochemistry, 16, 4743-4749 (1977)) was conducted to find that a mouse ADAMTS-1 cDNA labeled with ³²P by a random primed DNA-labeling kit (Boehringer Mannheim GmbH, Germany) was hybridized with the Flag. 1 DNA fragment. The results are shown in Fig. 3. A pCR™2.1 vector as a control was not hybridized with ³²P-labeled mouse ADAMTS-1 cDNA, whereas the mouse ADAMTS-1 cDNA and the Flag. 1 DNA fragment were hybridized with ³²P-labeled mouse ADAMTS-1 cDNA.

[0111] The results of the homology search and dot hybridization mean that the Flag. 1 DNA fragment is a part of the human ADAMTS-1.

[0112] To obtain a DNA fragment upstream of the Flag. 1 DNA fragment, a Rapid amplification of cDNA ends (RACE) method using a Marathon cDNA Amplification kit (Clontech Lab. Inc., Palo Alto, CA, USA) was performed as follows. That is, as back primers for the base sequence of the Flag. 1 DNA fragment, a DNA primer (hereinafter sometimes referred to as a "GSP-1 primer") having the base sequence (i.e., the base sequence of SEQ ID NO: 6: CCTCT-TAACT GCACTGTGTC AGT) complementary to the base sequence of the 3'-end region of the Flag. 1 DNA fragment, and a DNA primer (hereinafter sometimes referred to as a "GSP-2 primer") having the base sequence (i.e., the base sequence of SEQ ID NO: 7: CAGGCCCACT CCCAAAGGAA GCTT) complementary to the base sequence of the 5'-end region of the Flag. 1 DNA fragment were chemically synthesized. As forward primers, an AP1 primer and an AP2 primer attached to the above kit were used. The AP1 primer had the base sequence of SEQ ID NO: 8:

CCATCCTAAT ACGACTCACT ATAGGGC,

and the AP2 primer had the base sequence of SEQ ID NO: 9:

ACTCACTATA GGGCTCGAGC GGC.

[0113] After 5 µl of a human kidney cDNA library (Marathon-Ready cDNA; Clontech Lab. Inc., Palo Alto, CA, USA), 1 µl of the AP1 primer, 1 µl of 10 µM GSP-1 primer, 1 µl of a Tag polymerase (0.5 unit; Ex Taq polymerase), 1 µl of an anti-Taq polymerase antibody (Taq Start Antibody; Clontech Lab. Inc., Palo Alto, CA, USA), 5 µl of a PCR buffer having a 10-fold concentration [100mM Tris-HCl (pH 8.3), 500mM KCl] (Clontech Lab. Inc., Palo Alto, CA, USA), and 36 µl of distilled water were mixed, a PCR reaction was performed. The PCR reaction was carried out by repeating a cycle composed of a step at 94°C for 30 seconds and a step at 68°C for 4 minutes, 35 times, i.e., 35 cycles. The resulting reaction mixture was diluted to 50-fold with 10 mM Tricine-EDTA buffer (Clontech Lab. Inc., Palo Alto, CA, USA).

[0114] Then, 5 µl of the diluted liquid, 1 µl of the AP2 primer, 1 µl of a 10 µM GSP-2 primer, 1 µl of a Taq polymerase (0.5 unit; Ex Taq polymerase), 1 µl of an anti-Taq polymerase antibody (Taq Start Antibody), 5 µl of a PCR buffer having a 10-fold concentration (Clontech Lab. Inc., Palo Alto, CA, USA), and 36 µl of distilled water were mixed, and a PCR reaction was then performed. The PCR reaction was carried out by repeating a cycle composed of a step at 94°C for 30 seconds and a step at 68°C for 4 minutes 20 times, i.e., 20 cycles.

[0115] A sample (5 µl) was taken from the resulting reaction mixture, and electrophoresed on 1% agarose gel. As shown in Fig. 4, a single DNA band of about 1.2 Kb was observed. The DNA fragment (hereinafter sometimes referred to as a "Flag. 2 DNA fragment") was cloned in a pCR™ 2.1 vector by a conventional method, and the full-length base sequence of the Flag. 2 DNA fragment determined by a Dye Terminator Cycle Sequencing method (Perkin Elmer Japan, Urayasu, Japan).

[0116] Further, the full-length base sequence of the Flag. 1 DNA fragment was determined by the Dye Terminator Cycle Sequencing method (Perkin Elmer Japan, Urayasu, Japan). From the obtained base sequences of the Flag. 1 DNA fragment and the Flag. 2 DNA fragment, the full-length base sequence of the human ADAMTS-1 cDNA was determined. The full-length base sequence (2184 bp including a stop codon) is shown in SEQ ID NO: 2 and the amino acid sequence (727 amino acid residues) of the human ADAMTS-1 protein deduced from the above base sequence is shown in SEQ ID NO: 1. The partial base sequence of the Flag. 1 DNA fragment as shown in Fig. 2 contains some bases not identical to the full-length base sequence of the human ADAMTS-1 cDNA (SEQ ID NO: 2). However, the partial base sequence as shown in Fig. 2 was an interim sequence obtained in the process of determining the base sequence. The base sequence of SEQ ID NO: 2 is a correct base sequence of the human ADAMTS-1 cDNA which has been finally determined.

[0117] The human ADAMTS-1 protein is cysteine-rich, and contains many basic amino acids such as lysine and arginine in the C-terminal region, and two N-glycosylation sites (the 307th to 309th amino acids and 524th to 526th amino acids).

[0118] The homology between the base sequences of the human ADAMTS-1 gene and the mouse ADAMTS-1 gene is shown in Figs. 5 to 9, and the homology in the amino acid sequences deduced from the base sequences is shown in Figs. 10 to 12.

[0119] In Figs. 5 to 9, the symbol "" means that a base of the human ADAMTS-1 gene is identical to the corresponding base of the mouse ADAMTS-1 gene.

[0120] In Figs. 10 to 12, the symbol "" means that an amino acid residue of the human ADAMTS-1 protein is identical to the corresponding amino acid residue of the mouse ADAMTS-1 protein. In Figs. 10 to 12, "MMP domain" means a matrix metalloproteinase domain; the line between the 11th and 12th amino acids indicates the starting site of the matrix metalloproteinase domain; "DI domain" means the disintegrin domain; the line between the 234th and 235th amino acids indicates the starting site of the disintegrin domain; "TSP domain" means the thrombospondin domain; and amino acid sequences in boxes (three occurrences) mean the thrombospondin domain.

[0121] The homology in the base sequences between the human ADAMTS-1 and the mouse ADAMTS-1 was 85.5% and that in the amino acid sequences was 90.1%. The results show that ADAMTS-1 is the protein of which, between mouse and human, the sequences have been preserved.

Example 2: Preparation of the human ADAMTS-1 fusion protein in *E. coli*

(1) Construction of an expression vector for *E. coli*

[0122] To introduce a SmaI site at the 5'-side and a NotI site at the 3'-side into the DNA encoding a partial region downstream of the MMP domain in the full-length human ADAMTS-1 protein, a forward primer (2) having the base sequence of SEQ ID NO: 10:

CACCCCGGGA GGAAGAAGCG ATTTGTGTCC AGCCCCCGTT ATG,

and a back primer (2) having the base sequence of SEQ ID NO: 11:

GTGGCGGCCG CCCTCTTAAC TGCAGTGTGT CAGTGTGCAA AA

were chemically synthesized.

[0123] After 5 μ l of the forward primer (2), 5 μ l of the back primer (2), 1 μ l of a human kidney cDNA library (Marathon-Ready cDNA; Clontech Lab. Inc., Palo Alto, CA, USA), 1 μ l of a Taq polymerase (0.5 unit; Ex Taq polymerase), 1 μ l of an anti-Taq polymerase antibody (Taq Start Antibody; Clontech Lab. Inc., Palo Alto, CA, USA), 10 μ l of a PCR buffer having a 10-fold concentration (Clontech Lab. Inc., Palo Alto, CA, USA), 8 μ l of 2.5 mM 4dNTP (Takarashuzo, Kyoto, Japan), and 69 μ l of distilled water were mixed, a PCR reaction was performed. The PCR reaction was carried out by repeating a cycle composed of a step at 94°C for 1 minute, a step at 55°C for 45 seconds, and a step at 72°C for 2 seconds 40 times, i.e., 40 cycles.

[0124] A sample (5 μ l) was taken from the resulting reaction mixture, and electrophoresed on 1% agarose gel. As shown in Fig. 13, a single DNA band of about 2.2 Kb was obtained. The DNA fragment of about 2.2 Kb was cloned in the pCRTM 2.1 vector by a conventional method, and a large quantity of the plasmids produced [Nucleic Acids Res., 9, 2989-2998 (1981)]. The resulting plasmids prepared on a large scale were treated with restriction enzymes, SmaI (Takarashuzo, Kyoto, Japan) and NotI (Takarashuzo, Kyoto, Japan) to obtain a DNA fragment of about 2.2 Kb. The DNA fragment of about 2.2 Kb was cloned in a SmaI-NotI site of an expression vector for *E. coli* pGEX-5X-1 [Infect Immun., 58, 3909-3913 (1990)] (Pharmacia Biotech, Uppsala, Sweden). The resulting expression plasmid was named pG/ADAMTS-1. The structure of the plasmid pG/ADAMTS-1 is schematically shown in Fig. 14. It is believed that the ADAMTS-1 protein is expressed in the form of a fusion protein (molecular weight = about 96 Kd) with a glutathione-S-transferase (hereinafter sometimes referred to as a "GST") (molecular weight = about 26 Kd). In Fig. 14, "Ori" means a replication origin, "Amp^R" means an ampicillin resistance gene, and "Iaq I^R" means a Iaq repressor.

(2) Expression of the GST-human ADAMTS-1 fusion protein in *E. coli*

[0125] The plasmid pG/ADAMTS-1 was introduced into an *E. coli* BL-21 strain having a low protease activity (Pharmacia Biotech, Uppsala, Sweden) by a conventional method [Proc. Natl. Acad. Sci. USA, 69, 2110-2114 (1972)]. *E. coli* clones containing the plasmid were isolated as ampicillin resistance strains. Five ampicillin resistance strains (hereinafter referred to as "clone #1" to "clone #5") randomly selected from the strains were used to inoculate 2 ml of 2xYT medium (prepared by dissolving 16 g of trypton, 10 g of yeast extract, and 5g of NaCl in 1 liter of distilled water; pH 7.2), and cultured overnight at 37°C. Then, a set of two test tubes containing 1800 μ l of an LB culture medium containing ampicillin (100 μ g/ml) was prepared for each clone. To each test tube, 200 μ l of the overnight culture was poured. Then after incubating at 37°C for 2 hours, 20 μ l (final concentration = 1.0 mM) of isopropyl- β -D-thio-galactopyranoside (IPTG) (Takarashuzo, Tokyo, Japan), an expression-inducer, was added to one of the two test tubes. Thereafter, the test tubes were incubated at 37°C for 2 hours. The expression-inducer was not added to the other test tube, which was used as a control.

[0126] Microorganisms were harvested by centrifugation (14000 rpm, 1 minute) from 1 ml of the culture, using a microcentrifuging apparatus, then suspended in 100 μ l of a phosphate-buffered solution (140mM NaCl, 2.7mM KCl, 10mM Na₂ HPO₄, 1.8mM KH₂ PO₄, pH 7.2; hereinafter referred to as a PBS) and thereafter dissolved in 100 μ l of a 2 \times sample buffer (0.25M Tris-HCl, 2% SDS, 3% glycerol, 10% β -mercaptoethanol, 0.01% bromophenol blue; pH 6.8).
 5 The resulting solution (10 μ l) was subjected to an SDS-polyacrylamide gel electrophoresis (hereinafter sometimes referred to as an "SDS-PAGE"), and an expression induction of the desired protein was confirmed by a Coomassie staining method.

[0127] The results are shown in Fig. 15 wherein "+" lanes show the results of the electrophoresis of E coli incubated with the expression inducer, IPTG, and "-" lanes show the results of the electrophoresis of E coli incubated without the
 10 expression inducer, IPTG. In each "+" lane, a protein having a molecular weight of about 100 Kd was observed. This is identical to an expected molecular weight of the GST-human ADAMTS-1 fusion protein, i.e., about 96 Kd. However, such a protein was not observed in the "-" lanes.

[0128] Of five clones ("clone #1" to "clone #5"), the clone #2 exhibited the highest expression, and thus was used in the following Examples.

15 (3) Extraction and isolation of the GST-human ADAMTS-1 fusion protein

[0129] After overnight incubation, 1 ml of the culture of the clone #2 was added to 100 ml of a 2 \times YT culture medium containing 100 μ g/ml ampicillin, and incubated at 37°C. When an absorbance at 600 nm reached about 0.5, 1 ml of a
 20 100 mM IPTG was added to the culture, and then incubation was continued for 2 hours.

[0130] E. coli was harvested by centrifugation (3000 rpm, 30 minutes) from the culture, and then suspended in 8 ml of PBS. To the suspension, 1 ml of 0.5M EDTA solution and 1 ml of 25 mg/ml lysozyme solution were added, and the whole was allowed to stand in ice for 30 minutes. After 110 μ l of Triton X-100 was added, the microorganisms were disrupted on ice by a sonicator (TAITEC, Koshigaya, Japan). The disruption liquid was centrifuged (8000 rpm, 4°C, 10 min-
 25 utes), then the resulting precipitate suspended in 30 ml of PBS containing 1.0% Triton X-100, and thereafter centrifuged (8000 rpm, 4°C, 10 minutes).

[0131] The resulting precipitate was suspended in 2 ml of a 10 mM EDTA solution, and then, 50 ml of a 50 mM Tris-HCl buffer (pH 8.5) containing 8 M urea and 1% mercaptoethanol was added. After a thorough admixing, the mixture was centrifuged (15000 rpm, 4°C, 5 minutes). The resulting supernatant was dialyzed against 5 liters of a 10 mM Tris-HCl buffer (pH 8.5) at 4°C. The dialyzed solution was centrifuged (15000 rpm, 4°C, 5 minutes), and the resulting super-
 30 natant then adsorbed to an anion chromatography (Econo-Pac High Q; Bio-Rad Lab., Hercules, CA, USA). Fractions eluted with 0.2 to 0.4 M NaCl were dialyzed against 3 liters of PBS, and then adsorbed to 1 ml of glutathione Sepharose 4B (Pharmacia Biotech, Uppsala, Sweden) [Nucleic Acids Res., 9, 2989-2998 (1981)].

[0132] The glutathione Sepharose 4B was washed with 50 ml of PBS, and then eluted with 8 ml of 10 mM glutathione solution [Nucleic Acids Res., 9, 2989-2998 (1981)]. Fractions exhibiting a high GST activity detected by a GST
 35 detecting kit (Pharmacia Biotech, Uppsala, Sweden) were pooled.

[0133] A part of the fractions was subjected to an SDS-PAGE, and a Coomassie staining was performed. As shown in Fig. 16, a GST-human ADAMTS-1 fusion protein was confirmed from the molecular weight. The desired protein (about 1 μ g) was extracted and purified from 100 ml of E. coli culture.

40 [0134] The resulting fusion protein contains a site which may be broken with a Factor Xa or the like, between the GST and the human ADAMTS-1 protein, and therefore, the human ADAMTS-1 protein can be obtained by digesting the fusion protein with the proteinase. The human ADAMTS-1 protein may be used as an antigen to prepare an antibody.

45 Example 3: Examination of activities of GST-human ADAMTS-1 fusion protein on influencing hematopoietic functions

[0135] To examine the activities of the GST-human ADAMTS-1 fusion protein on influencing hematopoietic functions, a large-scale preparation of the GST-human ADAMTS-1 fusion protein was carried out in accordance with the process disclosed in Example 2 (3), and about 30 μ g of the desired protein was obtained from 3 liters of E. coli culture.

[0136] The functions thought to influence the number of blood cells by a single dosage of the GST-human
 50 ADAMTS-1 fusion protein to a tail vein of a mouse were examined, as the activities influencing hematopoietic functions. The examining system can be conducted with a small amount of a protein to be examined, and enables a quick elucidation of a biological activity. In a control test, a GST protein extracted and purified by the process disclosed in Example 2(3) from E. coli transformed with a vector pGEX-5X-1 was used.

[0137] The GST-human ADAMTS-1 fusion protein (1 μ g) was administered to eight C₅₇BL/6N mice (Charles river
 55 Japan, Yokohama, Japan) (male, 7 weeks old) at a tail vein. The numbers of leukocytes, erythrocytes, and platelets were counted 3 hours and 24 hours after the administration. In the control test, the GST protein (1 μ g) was administered to eight C₅₇BL/6N mice (Charles river Japan, Yokohama, Japan) (male, 7 weeks old) at a tail vein. The numbers of leukocytes, erythrocytes, and platelets were counted 3 hours and 24 hours after the administration.

[0138] The results are shown in Fig. 17. It is apparent from Fig. 17 that the number of leukocytes and platelets is significantly decreased, and the number of erythrocytes is significantly increased in the mice to which the GST-human ADAMTS-1 fusion protein was administered, in comparison with the control tests.

5 INDUSTRIAL APPLICABILITY

[0139] According to the protein of the present invention, hematopoietic functions can be controlled, for example, the number of leukocytes and platelets can be decreased, and at the same time, the number of erythrocytes can be increased.

10 [0140] As above, the present invention is explained with reference to particular embodiments, but modifications and improvements obvious to those skilled in the art are included in the scope of the present invention.

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SEQUENCE LISTING

5 SEQ ID NO: 1
 SEQUENCE LENGTH: 727
 SEQUENCE TYPE: amino acid
 10 SEQUENCE DESCRIPTION:
 Met Asp Ile Cys Arg Ile Arg Leu Arg Lys Lys Arg Phe Val Ser Ser
 5 10 15
 15 Pro Arg Tyr Val Glu Thr Met Leu Val Ala Asp Gln Ser Met Ala Glu
 20 25 30
 20 Phe His Gly Ser Gly Leu Lys His Tyr Leu Leu Thr Leu Phe Ser Val
 35 40 45
 Ala Ala Arg Leu Tyr Lys His Pro Ser Ile Arg Asn Ser Val Ser Leu
 25 50 55 60
 Val Val Val Lys Ile Leu Val Ile His Asp Glu Gln Lys Gly Pro Glu
 65 70 75 80
 30 Val Thr Ser Asn Ala Ala Leu Thr Leu Arg Asn Phe Cys Asn Trp Gln
 85 90 95
 35 Lys Gln His Asn Pro Pro Ser Asp Arg Asp Ala Glu His Tyr Asp Thr
 100 105 110
 Ala Ile Leu Phe Thr Arg Gln Asp Leu Cys Gly Ser Gln Thr Cys Asp
 40 115 120 125
 Thr Leu Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ser Arg Ser
 130 135 140
 45 Cys Ser Val Ile Glu Asp Asp Gly Leu Gln Ala Ala Phe Thr Thr Ala
 145 150 155 160
 50 His Glu Leu Gly His Val Phe Asn Met Pro His Asp Asp Ala Lys Gln
 165 170 175

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EP 1 004 674 A1

	Cys	Ala	Ser	Leu	Asn	Gly	Val	Asn	Gln	Asp	Ser	His	Met	Met	Ala	Ser	
5					180					185					190		
	Met	Leu	Ser	Asn	Leu	Asp	His	Ser	Gln	Pro	Trp	Ser	Pro	Cys	Ser	Ala	
					195					200					205		
10	Tyr	Met	Ile	Thr	Ser	Phe	Leu	Asp	Asn	Gly	His	Gly	Glu	Cys	Leu	Met	
					210					215					220		
15	Asp	Lys	Pro	Gln	Asn	Pro	Ile	Gln	Leu	Pro	Gly	Asp	Leu	Pro	Gly	Thr	
					225					230					235		240
	Leu	Tyr	Asp	Ala	Asn	Arg	Gln	Cys	Gln	Phe	Thr	Phe	Gly	Glu	Asp	Ser	
20					245					250					255		
	Lys	His	Cys	Pro	Asp	Ala	Ala	Ser	Thr	Cys	Ser	Thr	Leu	Trp	Cys	Thr	
25					260					265					270		
	Gly	Thr	Ser	Gly	Gly	Val	Leu	Val	Cys	Gln	Thr	Lys	His	Phe	Pro	Trp	
					275					280					275		
30	Ala	Asp	Gly	Thr	Ser	Cys	Gly	Glu	Gly	Lys	Trp	Cys	Ile	Asn	Gly	Lys	
					290					295					300		
35	Cys	Val	Asn	Lys	Thr	Asp	Arg	Lys	His	Phe	Asp	Thr	Pro	Phe	His	Gly	
					305					310					315		320
	Ser	Trp	Gly	Pro	Trp	Gly	Pro	Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	Gly	
40					325					330					335		
	Gly	Gly	Val	Gln	Tyr	Thr	Met	Arg	Glu	Cys	Asp	Asn	Pro	Val	Pro	Lys	
45					340					345					350		
	Asn	Gly	Gly	Lys	Tyr	Cys	Glu	Gly	Lys	Arg	Val	Arg	Tyr	Arg	Ser	Cys	
					355					360					365		
50	Asn	Leu	Glu	Asp	Cys	Pro	Asp	Asn	Asn	Gly	Lys	Thr	Phe	Arg	Glu	Glu	
					370					375					380		

EP 1 004 674 A1

	Gln Cys Glu Ala His Asn Glu Phe Ser Lys Ala Ser Phe Gly Ser Gly
5	385 390 395 400
	Pro Ala Val Glu Trp Ile Pro Lys Tyr Ala Gly Val Ser Pro Lys Asp
	405 410 415
10	Arg Cys Lys Leu Ile Cys Gln Ala Lys Gly Ile Gly Tyr Phe Phe Val
	420 425 430
15	Leu Gln Pro Lys Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser Thr
	435 440 445
	Ser Val Cys Val Gln Gly Gln Cys Val Lys Ala Gly Cys Asp Arg Ile
20	450 455 460
	Ile Asp Ser Lys Lys Lys Phe Asp Lys Cys Gly Val Cys Gly Gly Asn
25	465 470 475 480
	Gly Ser Thr Cys Lys Lys Ile Ser Gly Ser Val Thr Ser Ala Lys Pro
	485 490 495
30	Gly Tyr His Asp Ile Val Thr Ile Pro Thr Gly Ala Thr Asn Ile Glu
	500 505 510
35	Val Lys Gln Arg Asn Gln Arg Gly Ser Arg Asn Asn Gly Ser Phe Leu
	515 520 525
	Ala Ile Lys Ala Ala Asp Gly Thr Tyr Ile Leu Asn Gly Asp Tyr Thr
40	530 535 540
	Leu Ser Thr Leu Glu Gln Asp Ile Met Tyr Lys Gly Val Val Leu Arg
45	545 550 555 560
	Tyr Ser Gly Ser Ser Ala Ala Leu Glu Arg Ile Arg Ser Phe Ser Pro
	565 570 575
50	Leu Lys Glu Pro Leu Thr Ile Gln Val Leu Thr Val Gly Asn Ala Leu
	580 585 590
55	

EP 1 004 674 A1

Arg Pro Lys Ile Lys Tyr Thr Tyr Phe Val Lys Lys Lys Lys Glu Ser
5 595 600 605
Phe Asn Ala Ile Pro Thr Phe Ser Ala Trp Val Ile Glu Glu Trp Gly
610 615 620
10 Glu Cys Ser Lys Ser Cys Glu Leu Gly Trp Gln Arg Arg Leu Val Glu
625 630 635 640
15 Cys Arg Asp Ile Asn Gly Gln Pro Ala Ser Glu Cys Ala Lys Glu Val
645 650 655
Lys Pro Ala Ser Thr Arg Pro Cys Ala Asp His Pro Cys Pro Gln Trp
20 660 665 670
Gln Leu Gly Glu Trp Ser Ser Cys Ser Lys Thr Cys Gly Lys Gly Tyr
25 675 680 685
Lys Lys Arg Ser Leu Lys Cys Leu Ser His Asp Gly Gly Val Leu Ser
30 690 695 700
His Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Phe Ile Asp Phe
705 710 715 720
35 Cys Thr Leu Thr Gln Cys Ser
725

40
SEQ ID NO: 2
SEQUENCE LENGTH: 2184
45 SEQUENCE TYPE: nucleic acid
SEQUENCE DESCRIPTION:
ATG GAT ATC TGC AGA ATT CGG CTT AGG AAG AAG CGA TTT GTG TCC AGC 48
50 Met Asp Ile Cys Arg Ile Arg Leu Arg Lys Lys Arg Phe Val Ser Ser
5 10 15
55

EP 1 004 674 A1

	CCC CGT TAT GTG GAA ACC ATG CTT GTG GCA GAC CAG TCG ATG GCA GAA	96
5	Pro Arg Tyr Val Glu Thr Met Leu Val Ala Asp Gln Ser Met Ala Glu	
	20 25 30	
10	TTC CAC GGC AGT GGT CTA AAG CAT TAC CTT CTC ACG TTG TTT TCG GTG	144
	Phe His Gly Ser Gly Leu Lys His Tyr Leu Leu Thr Leu Phe Ser Val	
	35 40 45	
15	GCA GCC AGA TTG TAC AAA CAC CCC AGC ATT CGT AAT TCA GTT AGC CTG	192
	Ala Ala Arg Leu Tyr Lys His Pro Ser Ile Arg Asn Ser Val Ser Leu	
20	50 55 60	
	GTG GTG GTG AAG ATC TTG GTC ATC CAC GAT GAA CAG AAG GGG CCG GAA	240
25	Val Val Val Lys Ile Leu Val Ile His Asp Glu Gln Lys Gly Pro Glu	
	65 70 75 80	
	GTG ACC TCC AAT GCT GCC CTC ACT CTG CGG AAC TTT TGC AAC TGG CAG	288
30	Val Thr Ser Asn Ala Ala Leu Thr Leu Arg Asn Phe Cys Asn Trp Gln	
	85 90 95	
35	AAG CAG CAC AAC CCA CCC AGT GAC CGG GAT GCA GAG CAC TAT GAC ACA	336
	Lys Gln His Asn Pro Pro Ser Asp Arg Asp Ala Glu His Tyr Asp Thr	
40	100 105 110	
	GCA ATT CTT TTC ACC AGA CAG GAC TTG TGT GGG TCC CAG ACA TGT GAT	384
45	Ala Ile Leu Phe Thr Arg Gln Asp Leu Cys Gly Ser Gln Thr Cys Asp	
	115 120 125	
	ACT CTT GGG ATG GCT GAT GTT GGA ACT GTG TGT GAT CCG AGC AGA AGC	432
50	Thr Leu Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ser Arg Ser	
	130 135 140	

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EP 1 004 674 A1

	TGC TCC GTC ATA GAA GAT GAT GGT TTA CAA GCT GCC TTC ACC ACA GCC	480
5	Cys Ser Val Ile Glu Asp Asp Gly Leu Gln Ala Ala Phe Thr Thr Ala	
	145 150 155 160	
10	CAT GAA TTA GGC CAC GTG TTT AAC ATG CCA CAT GAT GAT GCA AAG CAG	528
	His Glu Leu Gly His Val Phe Asn Met Pro His Asp Asp Ala Lys Gln	
	165 170 175	
15	TGT GCC AGC CTT AAT GGT GTG AAC CAG GAT TCC CAC ATG ATG GCG TCA	576
	Cys Ala Ser Leu Asn Gly Val Asn Gln Asp Ser His Met Met Ala Ser	
20	180 185 190	
	ATG CTT TCC AAC CTG GAC CAC AGC CAG CCT TGG TCT CCT TGC AGT GCC	624
25	Met Leu Ser Asn Leu Asp His Ser Gln Pro Trp Ser Pro Cys Ser Ala	
	195 200 205	
30	TAC ATG ATT ACA TCA TTT CTG GAT AAT GGT CAT GGG GAA TGT TTG ATG	672
	Tyr Met Ile Thr Ser Phe Leu Asp Asn Gly His Gly Glu Cys Leu Met	
	210 215 220	
35	GAC AAG CCT CAG AAT CCC ATA CAG CTC CCA GGC GAT CTC CCT GGC ACC	720
	Asp Lys Pro Gln Asn Pro Ile Gln Leu Pro Gly Asp Leu Pro Gly Thr	
40	225 230 235 240	
	TTG TAC GAT GCC AAC CGG CAG TGC CAG TTT ACA TTT GGG GAG GAC TCC	768
	Leu Tyr Asp Ala Asn Arg Gln Cys Gln Phe Thr Phe Gly Glu Asp Ser	
45	245 250 255	
	AAA CAC TGC CCC GAT GCA GCC AGC ACA TGT AGC ACC TTG TGG TGT ACC	816
50	Lys His Cys Pro Asp Ala Ala Ser Thr Cys Ser Thr Leu Trp Cys Thr	
	260 265 270	
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EP 1 004 674 A1

	GGC ACC TCT GGT GGG GTG CTG GTG TGT CAA ACC AAA CAC TTC CCG TGG	864
5	Gly Thr Ser Gly Gly Val Leu Val Cys Gln Thr Lys His Phe Pro Trp	
	275 280 275	
10	GCG GAT GGC ACC AGC TGT GGA GAA GGG AAA TGG TGT ATC AAC GGC AAG	912
	Ala Asp Gly Thr Ser Cys Gly Glu Gly Lys Trp Cys Ile Asn Gly Lys	
	290 295 300	
15	TGT GTG AAC AAA ACC GAC AGG AAG CAT TTT GAT ACG CCT TTT CAT GGA	960
	Cys Val Asn Lys Thr Asp Arg Lys His Phe Asp Thr Pro Phe His Gly	
20	305 310 315 320	
	AGC TGG GGA CCA TGG GGA CCG TGG GGA GAC TGT TCG AGA ACG TGC GGT	1008
25	Ser Trp Gly Pro Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly	
	325 330 335	
30	GGA GGA GTC CAG TAC ACG ATG AGG GAA TGT GAC AAC CCA GTC CCA AAG	1056
	Gly Gly Val Gln Tyr Thr Met Arg Glu Cys Asp Asn Pro Val Pro Lys	
	340 345 350	
35	AAT GGA GGG AAG TAC TGT GAA GGC AAA CGA GTG CGC TAC AGA TCC TGT	1104
	Asn Gly Gly Lys Tyr Cys Glu Gly Lys Arg Val Arg Tyr Arg Ser Cys	
40	355 360 365	
	AAC CTT GAG GAC TGT CCA GAC AAT AAT GGA AAA ACC TTT AGA GAG GAA	1152
45	Asn Leu Glu Asp Cys Pro Asp Asn Asn Gly Lys Thr Phe Arg Glu Glu	
	370 375 380	
50	CAA TGT GAA GCA CAC AAC GAG TTT TCA AAA GCT TCC TTT GGG AGT GGG	1200
	Gln Cys Glu Ala His Asn Glu Phe Ser Lys Ala Ser Phe Gly Ser Gly	
	385 390 395 400	

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EP 1 004 674 A1

	CCT GCG GTG GAA TGG ATT CCC AAG TAC GCT GGC GTC TCA CCA AAG GAC	1248
5	Pro Ala Val Glu Trp Ile Pro Lys Tyr Ala Gly Val Ser Pro Lys Asp	
	405 410 415	
10	AGG TGC AAG CTC ATC TGC CAA GCC AAA GGC ATT GGC TAC TTC TTC GTT	1296
	Arg Cys Lys Leu Ile Cys Gln Ala Lys Gly Ile Gly Tyr Phe Phe Val	
	420 425 430	
15	TTG CAG CCC AAG GTT GTT GAT GGT ACT CCA TGT AGC CCA GAT TCC ACC	1344
	Leu Gln Pro Lys Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser Thr	
20	435 440 445	
	TCT GTC TGT GTG CAA GGA CAG TGT GTA AAA GCT GGT TGT GAT CGC ATC	1392
25	Ser Val Cys Val Gln Gly Gln Cys Val Lys Ala Gly Cys Asp Arg Ile	
	450 455 460	
30	ATA GAC TCC AAA AAG AAG TTT GAT AAA TGT GGT GTT TGC GGG GGA AAT	1440
	Ile Asp Ser Lys Lys Lys Phe Asp Lys Cys Gly Val Cys Gly Gly Asn	
	465 470 475 480	
35	GGA TCT ACT TGT AAA AAA ATA TCA GGA TCA GTT ACT AGT GCA AAA CCT	1488
	Gly Ser Thr Cys Lys Lys Ile Ser Gly Ser Val Thr Ser Ala Lys Pro	
40	485 490 495	
	GGA TAT CAT GAT ATC GTC ACA ATT CCA ACT GGA GCC ACC AAC ATC GAA	1536
45	Gly Tyr His Asp Ile Val Thr Ile Pro Thr Gly Ala Thr Asn Ile Glu	
	500 505 510	
50	GTG AAA CAG CCG AAC CAG AGG GGA TCC AGG AAC AAT GGC AGC TTT CTT	1584
	Val Lys Gln Arg Asn Gln Arg Gly Ser Arg Asn Asn Gly Ser Phe Leu	
	515 520 525	

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EP 1 004 674 A1

	GCC ATC AAA GCT GCT GAT GGC ACA TAT ATT CTT AAT GGT GAC TAC ACT	1632
5	Ala Ile Lys Ala Ala Asp Gly Thr Tyr Ile Leu Asn Gly Asp Tyr Thr	
	530 535 540	
10	TTG TCC ACC TTA GAG CAA GAC ATT ATG TAC AAA GGT GTT GTC TTG AGG	1680
	Leu Ser Thr Leu Glu Gln Asp Ile Met Tyr Lys Gly Val Val Leu Arg	
	545 550 555 560	
15	TAC AGC GGC TCC TCT GCG GCA TTG GAA AGA ATT CGC AGC TTT AGC CCT	1728
	Tyr Ser Gly Ser Ser Ala Ala Leu Glu Arg Ile Arg Ser Phe Ser Pro	
20	565 570 575	
	CTC AAA GAG CCC TTG ACC ATC CAG GTT CTT ACT GTG GGC AAT GCC CTT	1776
25	Leu Lys Glu Pro Leu Thr Ile Gln Val Leu Thr Val Gly Asn Ala Leu	
	580 585 590	
30	CGA CCT AAA ATT AAA TAC ACC TAC TTC GTA AAG AAG AAG AAG GAA TCT	1824
	Arg Pro Lys Ile Lys Tyr Thr Tyr Phe Val Lys Lys Lys Lys Glu Ser	
	595 600 605	
35	TTC AAT GCT ATC CCC ACT TTT TCA GCA TGG GTC ATT GAA GAG TGG GGC	1872
	Phe Asn Ala Ile Pro Thr Phe Ser Ala Trp Val Ile Glu Glu Trp Gly	
40	610 615 620	
	GAA TGT TCT AAG TCA TGT GAA TTG GGT TGG CAG AGA AGA CTG GTA GAA	1920
45	Glu Cys Ser Lys Ser Cys Glu Leu Gly Trp Gln Arg Arg Leu Val Glu	
	625 630 635 640	
50	TGC CGA GAC ATT AAT GGA CAG CCT GCT TCC GAG TGT GCA AAG GAA GTG	1968
	Cys Arg Asp Ile Asn Gly Gln Pro Ala Ser Glu Cys Ala Lys Glu Val	
	645 650 655	
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EP 1 004 674 A1

5 AAG CCA GCC AGC ACC AGA CCT TGT GCA GAC CAT CCC TGC CCC CAG TGG 2016
 Lys Pro Ala Ser Thr Arg Pro Cys Ala Asp His Pro Cys Pro Gln Trp
 660 665 670
 10 CAG CTG GGG GAG TGG TCA TCA TGT TCT AAG ACC TGT GGG AAG GGT TAC 2064
 Gln Leu Gly Glu Trp Ser Ser Cys Ser Lys Thr Cys Gly Lys Gly Tyr
 675 680 685
 15 AAA AAA AGA AGC TTG AAG TGT CTG TCC CAT GAT GGA GGG GTG TTA TCT 2112
 Lys Lys Arg Ser Leu Lys Cys Leu Ser His Asp Gly Gly Val Leu Ser
 690 695 700
 20 CAT GAG AGC TGT GAT CCT TTA AAG AAA CCT AAA CAT TTC ATA GAC TTT 2160
 His Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Phe Ile Asp Phe
 705 710 715 720
 25 TGC ACA CTG ACA CAG TGC AGT TAA 2184
 Cys Thr Leu Thr Gln Cys Ser
 30 725

35 SEQ ID NO: 3
 SEQUENCE LENGTH: 10
 SEQUENCE TYPE: amino acid
 SEQUENCE DESCRIPTION:
 40 Arg Thr Cys Gly Gly Gly Val Gln Tyr Thr
 5 10

45 SEQ ID NO: 4
 SEQUENCE LENGTH: 30
 SEQUENCE TYPE: nucleic acid
 50 SEQUENCE DESCRIPTION:
 AGAACCTGTG GTGGTGGAGT TCAATACACA 30

55

SEQ ID NO: 5

SEQUENCE LENGTH: 32

SEQUENCE TYPE: nucleic acid

SEQUENCE DESCRIPTION:

CCTCTTAACT GCACTGTGTC AGTGTGCAAA AG

32

SEQ ID NO: 6

SEQUENCE LENGTH: 23

SEQUENCE TYPE: nucleic acid

SEQUENCE DESCRIPTION:

CCTCTTAACT GCACTGTGTC AGT

23

SEQ ID NO: 7

SEQUENCE LENGTH: 24

SEQUENCE TYPE: nucleic acid

SEQUENCE DESCRIPTION:

CAGGCCCACT CCCAAAGGAA GCTT

24

SEQ ID NO: 8

SEQUENCE LENGTH: 27

SEQUENCE TYPE: nucleic acid

SEQUENCE DESCRIPTION:

CCATCCTAAT ACGACTCACT ATAGGCC

27

SEQ ID NO: 9

SEQUENCE LENGTH: 23

SEQUENCE TYPE: nucleic acid

SEQUENCE DESCRIPTION:

ACTCACTATA GGGCTCGAGC GGC

23

SEQ ID NO: 10

SEQUENCE LENGTH: 43

SEQUENCE TYPE: nucleic acid

SEQUENCE DESCRIPTION:

CACCCCGGGA GGAAGAAGCG ATTTGTGTCC AGCCCCCGTT ATG

43

SEQ ID NO: 11

SEQUENCE LENGTH: 42

SEQUENCE TYPE: nucleic acid

SEQUENCE DESCRIPTION:

GTGGCGGCCG CCCTCTTAAC TGCCTGTGT CAGTGTGCAA AA

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Claims

1. A protein characterized by containing an amino acid sequence of SEQ ID NO: 1:

EP 1 004 674 A1

Met Asp Ile Cys Arg Ile Arg Leu Arg Lys Lys Arg Phe Val Ser Ser
 5 Pro Arg Tyr Val Glu Thr Met Leu Val Ala Asp Gln Ser Met Ala Glu
 Phe His Gly Ser Gly Leu Lys His Tyr Leu Leu Thr Leu Phe Ser Val
 10 Ala Ala Arg Leu Tyr Lys His Pro Ser Ile Arg Asn Ser Val Ser Leu
 Val Val Val Lys Ile Leu Val Ile His Asp Glu Gln Lys Gly Pro Glu
 Val Thr Ser Asn Ala Ala Leu Thr Leu Arg Asn Phe Cys Asn Trp Gln
 15 Lys Gln His Asn Pro Pro Ser Asp Arg Asp Ala Glu His Tyr Asp Thr
 Ala Ile Leu Phe Thr Arg Gln Asp Leu Cys Gly Ser Gln Thr Cys Asp
 20 Thr Leu Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ser Arg Ser
 Cys Ser Val Ile Glu Asp Asp Gly Leu Gln Ala Ala Phe Thr Thr Ala
 25 His Glu Leu Gly His Val Phe Asn Met Pro His Asp Asp Ala Lys Gln
 Cys Ala Ser Leu Asn Gly Val Asn Gln Asp Ser His Met Met Ala Ser
 Met Leu Ser Asn Leu Asp His Ser Gln Pro Trp Ser Pro Cys Ser Ala
 30 Tyr Met Ile Thr Ser Phe Leu Asp Asn Gly His Gly Glu Cys Leu Met
 Asp Lys Pro Gln Asn Pro Ile Gln Leu Pro Gly Asp Leu Pro Gly Thr
 35 Leu Tyr Asp Ala Asn Arg Gln Cys Gln Phe Thr Phe Gly Glu Asp Ser
 Lys His Cys Pro Asp Ala Ala Ser Thr Cys Ser Thr Leu Trp Cys Thr
 40 Gly Thr Ser Gly Gly Val Leu Val Cys Gln Thr Lys His Phe Pro Trp
 Ala Asp Gly Thr Ser Cys Gly Glu Gly Lys Trp Cys Ile Asn Gly Lys
 45 Cys Val Asn Lys Thr Asp Arg Lys His Phe Asp Thr Pro Phe His Gly
 Ser Trp Gly Pro Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly
 Gly Gly Val Gln Tyr Thr Met Arg Glu Cys Asp Asn Pro Val Pro Lys
 50 Asn Gly Gly Lys Tyr Cys Glu Gly Lys Arg Val Arg Tyr Arg Ser Cys

Asn Leu Glu Asp Cys Pro Asp Asn Asn Gly Lys Thr Phe Arg Glu Glu
 5 Gln Cys Glu Ala His Asn Glu Phe Ser Lys Ala Ser Phe Gly Ser Gly
 Pro Ala Val Glu Trp Ile Pro Lys Tyr Ala Gly Val Ser Pro Lys Asp
 Arg Cys Lys Leu Ile Cys Gln Ala Lys Gly Ile Gly Tyr Phe Phe Val
 10 Leu Gln Pro Lys Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser Thr
 Ser Val Cys Val Gln Gly Gln Cys Val Lys Ala Gly Cys Asp Arg Ile
 15 Ile Asp Ser Lys Lys Lys Phe Asp Lys Cys Gly Val Cys Gly Gly Asn
 Gly Ser Thr Cys Lys Lys Ile Ser Gly Ser Val Thr Ser Ala Lys Pro
 20 Gly Tyr His Asp Ile Val Thr Ile Pro Thr Gly Ala Thr Asn Ile Glu
 Val Lys Gln Arg Asn Gln Arg Gly Ser Arg Asn Asn Gly Ser Phe Leu
 Ala Ile Lys Ala Ala Asp Gly Thr Tyr Ile Leu Asn Gly Asp Tyr Thr
 25 Leu Ser Thr Leu Glu Gln Asp Ile Met Tyr Lys Gly Val Val Leu Arg
 Tyr Ser Gly Ser Ser Ala Ala Leu Glu Arg Ile Arg Ser Phe Ser Pro
 30 Leu Lys Glu Pro Leu Thr Ile Gln Val Leu Thr Val Gly Asn Ala Leu
 Arg Pro Lys Ile Lys Tyr Thr Tyr Phe Val Lys Lys Lys Lys Glu Ser
 35 Phe Asn Ala Ile Pro Thr Phe Ser Ala Trp Val Ile Glu Glu Trp Gly
 Glu Cys Ser Lys Ser Cys Glu Leu Gly Trp Gln Arg Arg Leu Val Glu
 40 Cys Arg Asp Ile Asn Gly Gln Pro Ala Ser Glu Cys Ala Lys Glu Val
 Lys Pro Ala Ser Thr Arg Pro Cys Ala Asp His Pro Cys Pro Gln Trp
 45 Gln Leu Gly Glu Trp Ser Ser Cys Ser Lys Thr Cys Gly Lys Gly Tyr
 Lys Lys Arg Ser Leu Lys Cys Leu Ser His Asp Gly Gly Val Leu Ser
 His Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Phe Ile Asp Phe
 50 Cys Thr Leu Thr Gln Cys Ser.

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2. A variation functionally equivalent to a protein containing an amino acid sequence of SEQ ID NO: 1.
 3. A protein characterized by containing a matrix metalloproteinase domain, a disintegrin domain, and a throm-

EP 1 004 674 A1

bospondin domain, except for a mouse ADAMTS-1 protein.

4. A gene characterized by encoding said protein according to any one of claims 1 to 3.

5 5. A gene containing a base sequence of SEQ ID NO: 2:

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EP 1 004 674 A1

5 ATG GAT ATC TGC AGA ATT CGG CTT AGG AAG AAG CGA TTT GTG TCC AGC
 CCC CGT TAT GTG GAA ACC ATG CTT GTG GCA GAC CAG TCG ATG GCA GAA
 TTC CAC GGC AGT GGT CTA AAG CAT TAC CTT CTC ACG TTG TTT TCG GTG
 10 GCA GCC AGA TTG TAC AAA CAC CCC AGC ATT CGT AAT TCA GTT AGC CTG
 GTG GTG GTG AAG ATC TTG GTC ATC CAC GAT GAA CAG AAG GGG CCG GAA
 GTG ACC TCC AAT GCT GCC CTC ACT CTG CGG AAC TTT TGC AAC TGG CAG
 15 AAG CAG CAC AAC CCA CCC AGT GAC CGG GAT GCA GAG CAC TAT GAC ACA
 GCA ATT CTT TTC ACC AGA CAG GAC TTG TGT GGG TCC CAG ACA TGT GAT
 20 ACT CTT GGG ATG GCT GAT GTT GGA ACT GTG TGT GAT CCG AGC AGA AGC
 TGC TCC GTC ATA GAA GAT GAT GGT TTA CAA GCT GCC TTC ACC ACA GCC
 CAT GAA TTA GGC CAC GTG TTT AAC ATG CCA CAT GAT GAT GCA AAG CAG
 25 TGT GCC AGC CTT AAT GGT GTG AAC CAG GAT TCC CAC ATG ATG GCG TCA
 ATG CTT TCC AAC CTG GAC CAC AGC CAG CCT TGG TCT CCT TGC AGT GCC
 30 TAC ATG ATT ACA TCA TTT CTG GAT AAT GGT CAT GGG GAA TGT TTG ATG
 GAC AAG CCT CAG AAT CCC ATA CAG CTC CCA GGC GAT CTC CCT GGC ACC
 35 TTG TAC GAT GCC AAC CGG CAG TGC CAG TTT ACA TTT GGG GAG GAC TCC
 AAA CAC TGC CCC GAT GCA GCC AGC ACA TGT AGC ACC TTG TGG TGT ACC
 40 GGC ACC TCT GGT GGG GTG CTG GTG TGT CAA ACC AAA CAC TTC CCG TGG
 GCG GAT GGC ACC AGC TGT GGA GAA GGG AAA TGG TGT ATC AAC GGC AAG
 TGT GTG AAC AAA ACC GAC AGG AAG CAT TTT GAT ACG CCT TTT CAT GGA
 45 AGC TGG GGA CCA TGG GGA CCG TGG GGA GAC TGT TCG AGA ACG TGC GGT
 GGA GGA GTC CAG TAC ACG ATG AGG GAA TGT GAC AAC CCA GTC CCA AAG
 50 AAT GGA GGG AAG TAC TGT GAA GGC AAA CGA GTG CGC TAC AGA TCC TGT
 AAC CTT GAG GAC TGT CCA GAC AAT AAT GGA AAA ACC TTT AGA GAG GAA
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CAA TGT GAA GCA CAC AAC GAG TTT TCA AAA GCT TCC TTT GGG AGT GGG
 5 CCT GCG GTG GAA TGG ATT CCC AAG TAC GCT GGC GTC TCA CCA AAG GAC
 AGG TGC AAG CTC ATC TGC CAA GCC AAA GGC ATT GGC TAC TTC TTC GTT
 10 TTG CAG CCC AAG GTT GTT GAT GGT ACT CCA TGT AGC CCA GAT TCC ACC
 TCT GTC TGT GTG CAA GGA CAG TGT GTA AAA GCT GGT TGT GAT CGC ATC
 ATA GAC TCC AAA AAG AAG TTT GAT AAA TGT GGT GTT TGC GGG GGA AAT
 15 GGA TCT ACT TGT AAA AAA ATA TCA GGA TCA GTT ACT AGT GCA AAA CCT
 GGA TAT CAT GAT ATC GTC ACA ATT CCA ACT GGA GCC ACC AAC ATC GAA
 20 GTG AAA CAG CGG AAC CAG AGG GGA TCC AGG AAC AAT GGC AGC TTT CTT
 GCC ATC AAA GCT GCT GAT GGC ACA TAT ATT CTT AAT GGT GAC TAC ACT
 25 TTG TCC ACC TTA GAG CAA GAC ATT ATG TAC AAA GGT GTT GTC TTG AGG
 TAC AGC GGC TCC TCT GCG GCA TTG GAA AGA ATT CGC AGC TTT AGC CCT
 CTC AAA GAG CCC TTG ACC ATC CAG GTT CTT ACT GTG GGC AAT GCC CTT
 30 CGA CCT AAA ATT AAA TAC ACC TAC TTC GTA AAG AAG AAG AAG GAA TCT
 TTC AAT GCT ATC CCC ACT TTT TCA GCA TGG GTC ATT GAA GAG TGG GGC
 35 GAA TGT TCT AAG TCA TGT GAA TTG GGT TGG CAG AGA AGA CTG GTA GAA
 TGC CGA GAC ATT AAT GGA CAG CCT GCT TCC GAG TGT GCA AAG GAA GTG
 40 AAG CCA GCC AGC ACC AGA CCT TGT GCA GAC CAT CCC TGC CCC CAG TGG
 CAG CTG GGG GAG TGG TCA TCA TGT TCT AAG ACC TGT GGG AAG GGT TAC
 45 AAA AAA AGA AGC TTG AAG TGT CTG TCC CAT GAT GGA GGG GTG TTA TCT
 CAT GAG AGC TGT GAT CCT TTA AAG AAA CCT AAA CAT TTC ATA GAC TTT
 50 TGC ACA CTG ACA CAG TGC AGT TAA.

6. A vector characterized by containing said gene according to claim 4 or 5.
7. A transformant characterized by being transformed by said vector according to claim 6.
8. A pharmaceutical composition characterized by comprising

EP 1 004 674 A1

- (1) a protein containing an amino acid sequence of SEQ ID NO: 1,
(2) a variation functionally equivalent to said protein containing said amino acid sequence of SEQ ID NO: 1, or
(3) a protein containing a matrix metalloproteinase domain, a disintegrin domain, and a thrombospondin domain, and
a pharmaceutically or veterinarily acceptable carrier.

9. The pharmaceutical composition according to claim 8, for reducing leukocytes.

10. The pharmaceutical composition according to claim 8, for reducing platelets.

11. The pharmaceutical composition according to claim 8, for increasing erythrocytes.

12. A food characterized by comprising

- (1) a protein containing an amino acid sequence of SEQ ID NO: 1,
(2) a variation functionally equivalent to said protein containing said amino acid sequence of SEQ ID NO: 1, or
(3) a protein containing a matrix metalloproteinase domain, a disintegrin domain, and a thrombospondin domain, and a food additive.

13. A food additive characterized by comprising

- (1) a protein containing an amino acid sequence of SEQ ID NO: 1,
(2) a variation functionally equivalent to said protein containing said amino acid sequence of SEQ ID NO: 1, or
(3) a protein containing a matrix metalloproteinase domain, a disintegrin domain, and a thrombospondin domain.

14. An immunologically reactive substance characterized by being reactive specifically to said protein according to any one of claims 1 to 3.

15. A method for immunologically analyzing a human ADAMTS-1 protein containing an amino acid sequence of SEQ ID NO: 1, characterized in that a sample is brought into contact with an immunologically reactive substance which is reactive specifically to said human ADAMTS-1 protein, and a complex of said human ADAMTS-1 protein and said immunologically reactive substance is detected.

16. A method for extracorporeally detecting an immunological state, characterized by analyzing a human ADAMTS-1 protein containing an amino acid sequence of SEQ ID NO: 1 in a sample.

17. A method for immunologically analyzing an mRNA of a human ADAMTS-1 protein containing an amino acid sequence of SEQ ID NO: 1, characterized in that a sample is brought into contact with a polynucleotide containing a base sequence complementary to that of said mRNA of said human ADAMTS-1 protein, and a complex of said mRNA of said human ADAMTS-1 protein and said gene is detected.

18. A method for extracorporeally detecting an immunological state, characterized by analyzing an mRNA of a human ADAMTS-1 protein containing an amino acid sequence of SEQ ID NO: 1 in a sample.

19. An agent for analyzing an immunological state, characterized by containing an immunologically reactive substance capable of immunologically reacting a human ADAMTS-1 protein containing an amino acid sequence of SEQ ID NO: 1.

20. An agent for analyzing an immunological state, characterized by containing a polynucleotide containing a base sequence complementary to that of an mRNA of a human ADAMTS-1 protein containing an amino acid sequence of SEQ ID NO: 1.

21. A method for reducing leukocytes, comprising administering to a subject in need thereof,

- (1) a protein containing an amino acid sequence of SEQ ID NO: 1,
(2) a variation functionally equivalent to said protein containing said amino acid sequence of SEQ ID NO: 1, or
(3) a protein containing a matrix metalloproteinase domain, a disintegrin domain, and a thrombospondin

domain,
an an amount effective therefor.

22. A method for reducing platelets, comprising administering to a subject in need thereof,

5

- (1) a protein containing an amino acid sequence of SEQ ID NO: 1,
 - (2) a variation functionally equivalent to said protein containing said amino acid sequence of SEQ ID NO: 1, or
 - (3) a protein containing a matrix metalloproteinase domain, a disintegrin domain, and a thrombospondin domain,
- in an amount effective therefor.

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23. A method for increasing erythrocytes, comprising administering to a subject in need thereof,

15

- (1) a protein containing an amino acid sequence of SEQ ID NO: 1,
 - (2) a variation functionally equivalent to said protein containing said amino acid sequence of SEQ ID NO: 1, or
 - (3) a protein containing a matrix metalloproteinase domain, a disintegrin domain, and a thrombospondin domain,
- in an amount effective therefor.

20 24. Use of

25

- (1) a protein containing an amino acid sequence of SEQ ID NO: 1,
 - (2) a variation functionally equivalent to said protein containing said amino acid sequence of SEQ ID NO: 1, or
 - (3) a protein containing a matrix metalloproteinase domain, a disintegrin domain, and a thrombospondin domain,
- for preparing a pharmaceutical composition.

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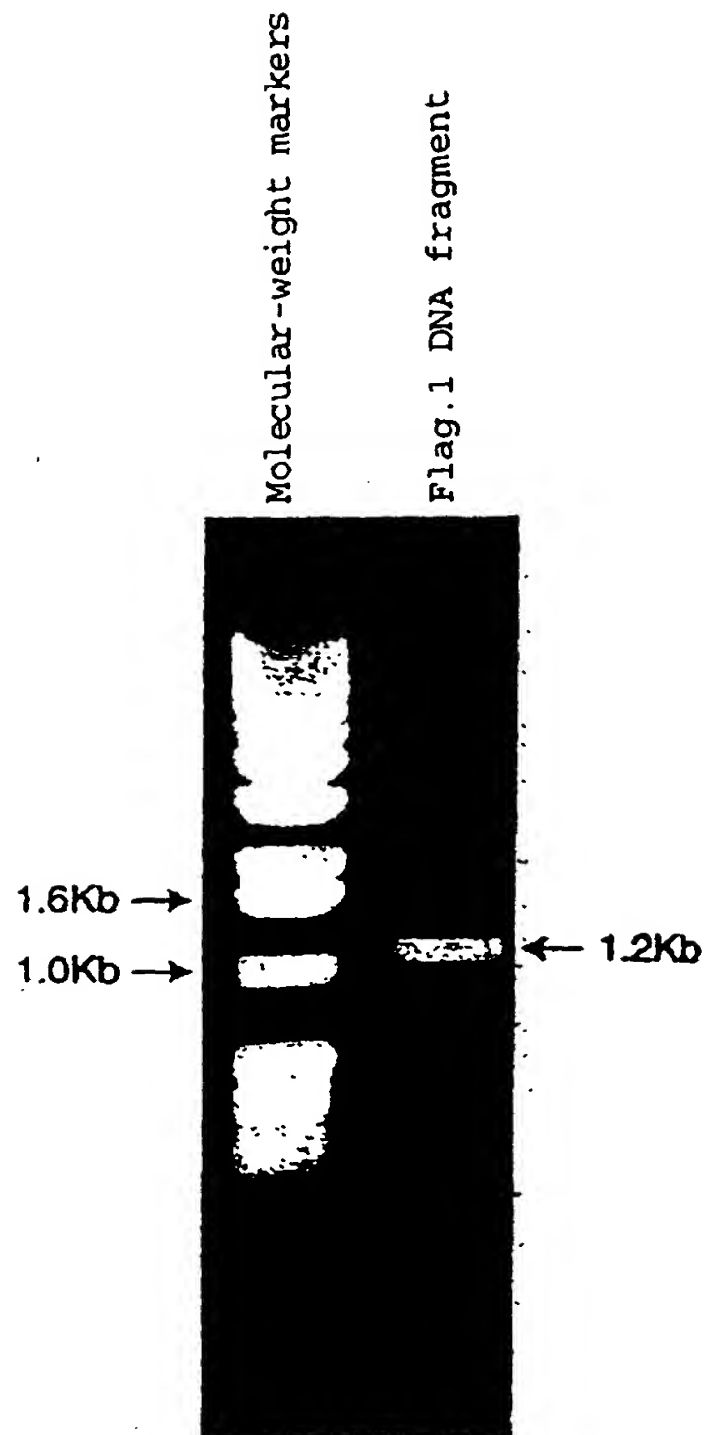
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FIG. 1



Mouse ADAMTS-1
Frag.1

2101 ACTGCTCAAGAACCTGTGGTGGAGTTCAATACACAATGAGAGAA GTGACAACCAG
::: :
1 CAAGAACCCTGTGGTGGAGTTCAATTACAGATGAGGATTGTTACAACCAG
2161 TCCCAAAGAACGGGAAGTACTGTGAAGGCCAACGAGTCCGCTACAGGTCCTGTAACA
::: :
55 TCCCAAAGATTGGAGGGAAGTCTTGTAAGGCCAACGAGTGCCCTACAGTTCCTTTATCG
2221 TCGAGGACTGTCCAGACAATAACGGAAAACG--TTCAGAGAGGAGCAGTGGGAGGCG-C
:
115 TTTAGGACTGTCTAGACAATTACTGGAATTCGACTTAAGAGTGGCCCA-T CCTATGCGGC
2278 ACAATGAGTTTTCCAAGCTTCCTTTGGGAATGAGCCCACGTIAG-AGTGG-ACACCCAA
:: :
174 ACACCGGTTTCAAAATGTTTCCCTTTGGGAGTTGGGCTGCGGTGGAATTGGTTTTCCCAA
2336 GTACCGCGCGTCTCGCCAAAGGACAGGTGCAAGCTCA-CCTGTGAAGCCAAAGGCATTG
:
234 GGATCGTGGCGTCTACCCAAAGGACAGGTGCAAGCTCATGCCAAAGCCAAAGG-ATTG
2395 GCTACTTTTTTCGTCTTACAGCCCCAAGGTTGTAGATGGCACCTCCCTGTAGTCCAGACTCTA
:::: :
293 GCTACATTTTC

FIG. 2

FIG. 3

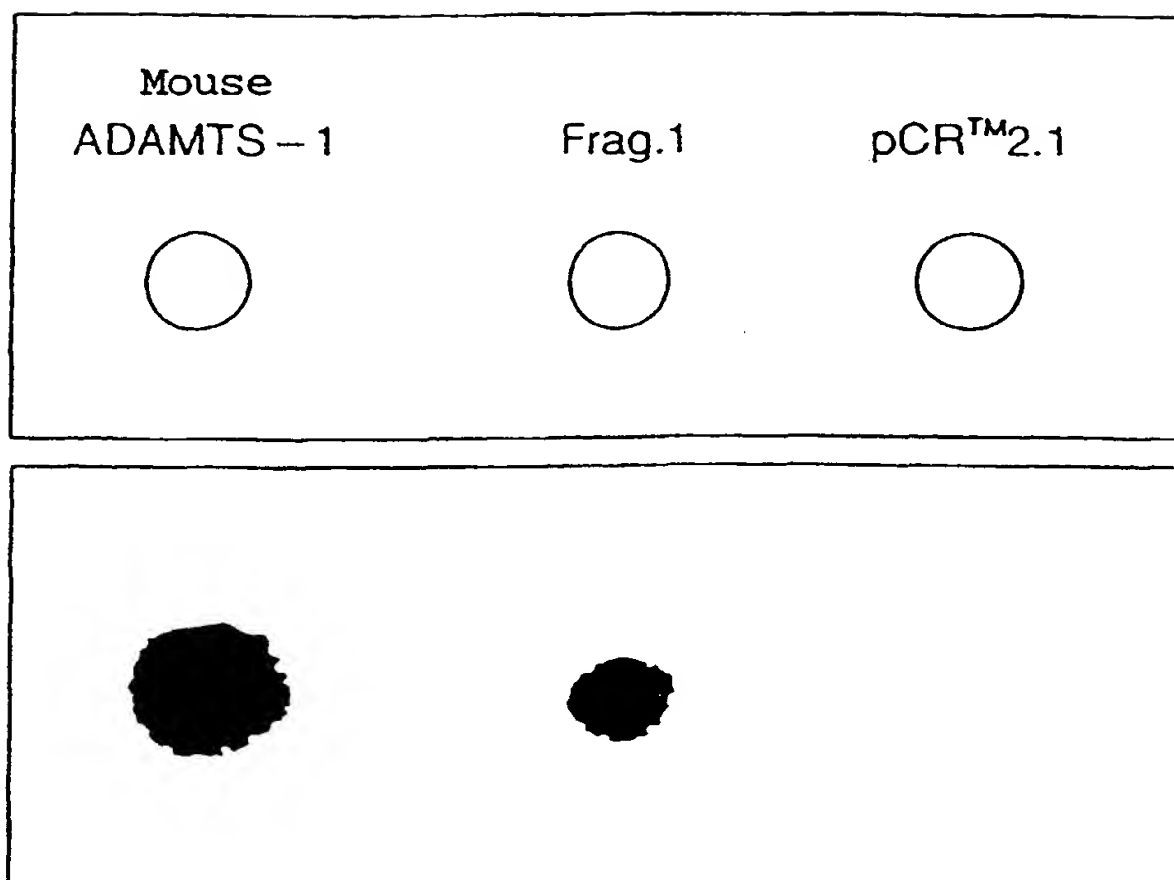
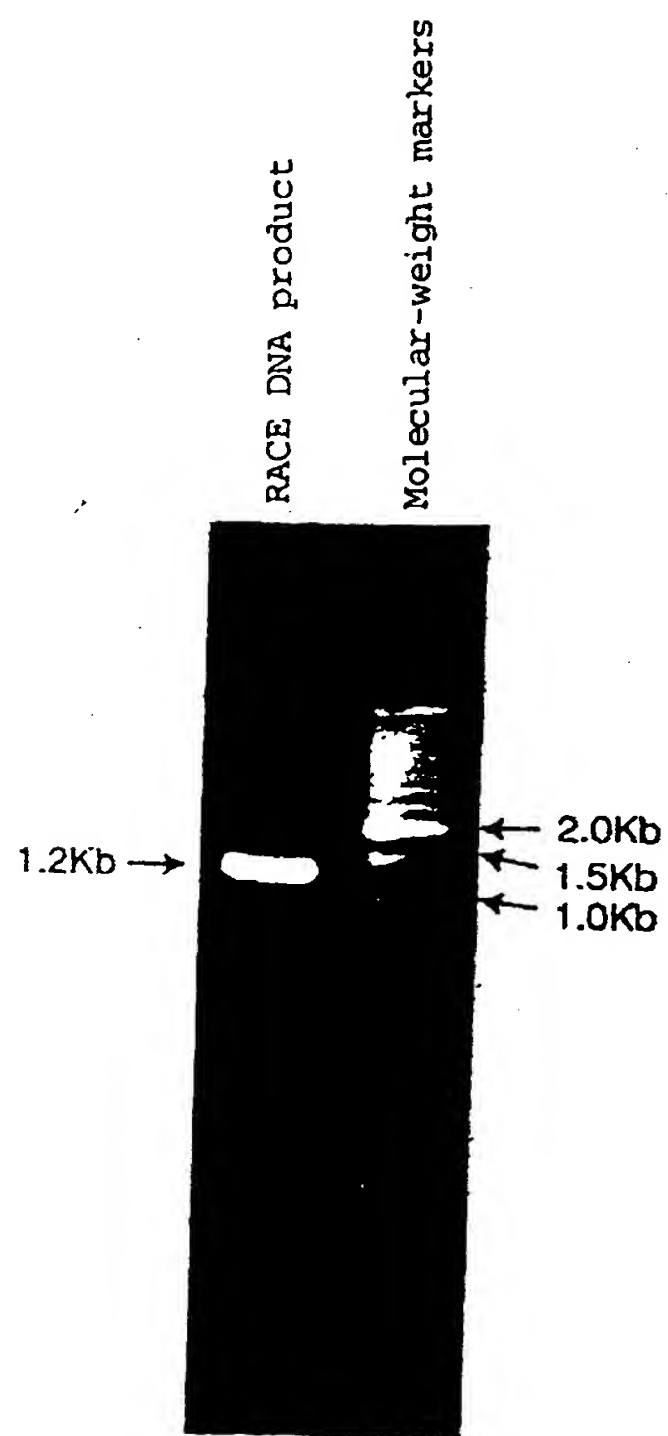


FIG. 4



F I G. 5

Hu ADAMTS-1 1' ATGGATATCTGCAGAAATTCGGCTTAGGAAGAAAGCGATTTGTGTCCAGCCCCCGTTATGTG
* * * * *
Mu ADAMTS-1 1" AAGCCATCAGGACCAGGAAGCATAAAGGAAGAAAGCGATTTGTGTCCAGCCCCCGTTATGTG
* * * * *

61' GAAACCATGCTTGTGGCAGACCAGTCGATGGCAGAAATTCACGGGCAGTGGTCTAAAGCAT
* * * * *
61" GAAACCATGCTCGTAGCTGACCAGTCCTCATGGCCGACTTCCACGGGCAGCGGTCTAAAGCAT
* * * * *

121' TACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTTGTACAAACACCCAGCATTCGTAAT
* * * * *
121" TACCTTCTAACCCCTGTTCTCGGTGGCAGCCAGGTTTACAAAGCATCCAGCATTAGGAAT
* * * * *

181' TCAGTTAGCCTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAAGGGCCGGAA
* * * * *
181" TCAATTAGCCTGGTGGTGAAGATCTTGGTCATATACGAGGAGCAGAAAGGGACCAGAA
* * * * *

241' GTGACCTCCAATGCTGCCCTCACTCTGCGGAACCTTTGCAACTGGCAGAAAGCAGCACAAAC
* * * * *
241" GTTACCTCCAATGCAGCTCTCACCCCTTCGGGAATTTCTGCAGCTGGCAGAAACACAAAC
* * * * *

301' CCACCCAGTGACCGGGATGCAGAGCAGCACTATGACACAGCAATTTCTTTCACCCAGACAGGAC
* * * * *
301" AGCCCCAGTGACCGGGATCCAGAGCAGCACTATGACACAGCAATTTCTGTTCACCCAGACAGGAT
* * * * *

361' TTGTGTGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACTGTGTGTGAT
* * * * *
361" TTATGTGGTCCCACACACGCTGTGACACTCTCGGAATGGCAGATGTTGGAACTGTGTGAT
* * * * *

421' CCGAGCAGAAAGCTGCTCCGTCATAGAAAGATGATGGTTTACAAGCTGCCCTTCACCCAGGCC
* * * * *
421" CCGAGCAGGAGCTGCTCAGTCATAGAAAGATGATGGTTTGCAGCTGCCCTTCACCCAGGCC
* * * * *

F I G. 6

Hu ADAMTS-1 481' CATGAATTAGGCCACGTTTAAACATGCCACATGATGCAAGCAGTGTGCCAGCCTT

Mu ADAMTS-1 481" CATGAATTGGGCCATGTGTTTAAACATGCCACGATGCTAAGCACTGTGCCAGCTTG

541' AATGGTGTGAACCAGGATTCCCCACATGATGGCGTCAATGCTTTCCAAACCTGGACACAGC

541" AATGGTGTGAGTGGCGATTCTCATCTGATGGCCCTCGATGCTCTCCAGCTTAGACCATAGC

601' CAGCCTTGGTCTCCTTGCAGTGCCCTACATGATTACATCATTTCTGGATAATGGTCAATGGG

601" CAGCCCTGGTCACCTTGCAGTGCCCTACATGGTCACGYCCTTCCCTAGATAATGGACACGGG

661' GAATGTTTGATGGACAAGCCCTCAGAAATCCCATACAGCTCCAGGCGATCTCCCTGGCACCC

661" GAATGTTTGATGGACAAGCCCCAGAAATCCAAATCAAGCTCCCTTCTGATCTTCCCGGTACC

721' TTGTACGATGCCAAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCCC

721" TTGTACGATGCCAAACCGCCAGTGTCAGTTTACATTCGGAGAGGAATCCAAGCACTGCCCT

781' GATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGGTGCTGGTG

781" GATGCAGCCAGCACATGTACTACCCCTGTGGTGCACCTCCGGTGGCTTACTGGTG

841' TGTCAAACCAAACACTTCCCGTGGCGGATGGCCACCAAGCTGTGGAGAGGGAATGGTGT

841" TGCCAAACCAAACACTTCCCTTGGGCAGATGGCCACCAAGCTGTGGAGAGGGAAGTGGTG

901' ATCAACGGCAAGTGTGTGAACAAACCGACAGGAAGCATTTTGATACGCCCTTTTCATGGA

901" GTCAAGTGGCAAGTGGGTGAACAAAGACAGACATGAAGCATTTTGCTACTCCTGTTTCATGGA

FIG. 7

Hu ADAMTS-1	961'	AGCTGGGGACCATGGGGACCGTGGGGAGACTGTTTCGAGAACGTGCGGTGGAGGAGTCCAG

Mu ADAMTS-1	961"	AGCTGGGGACCATGGGGACCGTGGGGAGACTGCTCAAGAACCTGTGGTGGTGGAGTTCAA

	1021'	TACACGATGAGGGAATGTGACAACCCAGTCCCAAGAAATGGAGGGAAGTACTGTGAAGGC

	1021"	TACACAAATGAGAGAAATGTGACAACCCAGTCCCAAGAACGGGGAAGTACTGTGAAGGC

	1081'	AAACGAGTGGCGTACAGATCCTGTAAACCTTGAGGACTGTCCAGACAAATAATGGAAAAACC

	1081"	AAACGAGTCCGCTACAGGTCTGTAAACATCGAGGACTGTCCAGACAAATAACGGAAAAACG

	1141'	TTTAGAGAGGAACAATGTGAAGCACACACGAGTTTTCAAAAGCTTCTTTGGGAGTGGG

	1141"	TTCAGAGAGGAGCAGTGGAGGCGCACAAATGAGTTTCCAAAGCTTCTTTGGGAATGAG

	1201'	CTGCGGTGGAAATGGATTCCCAAGTACGCTGGCGTCTCACCAAGGACAGGTGCCAAGCTC

	1201"	CCCACTGTAGAGTGGACACCCAAAGTACGCCGCGTCTCGCCAAAGGACAGGTGCCAAGCTC

	1261'	ATCTGCCAAGCCAAAGGCAATTGGCTACTTCTTCGTTTTCGAGCCCAAGGTTGTGATGGT

	1261"	ACCTGTGAAGCCAAAGGCAATTGGCTACTTTTCGTCTTACAGCCCAAGGTTGTAGATGGC

	1321'	ACTCCATGTAGCCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAAGCTGGT

	1321"	ACTCCCTGTAGTCCAGACTCTACCTCTGTCTGTGTGCAAGGGCAGTGTGTGAAGCTGGC

	1381'	TGTGATCGCATCATAGACTCCAAAAAGAAAGTTTGATAAAATGTGGTGTTCGGGGGAAAT

	1381"	TGTGATCGCATCATAGACTCCAAAAAGAAAGTTTGATAAGTGTGGCGTTTGTGGAGGAAC

F I G. 8

Hu ADAMTS-1 1441' GGATCTACTTGTAAATAATATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGAT
**
Mu ADAMTS-1 1441" GGTTCCACATGCAAGAAGATGTCAGGAATAGTCACTAGTACAAGACCTGGGTATCATGAC
1501' ATCGTCACAATTCCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAACCCAGAGGGGA
** ** ** ** ** ** ** ** ** ** **
1501" ATGTCAACAATTCCCTGCTGGAGCCACCAACATTTGAAGTGAAACATCGGAATCAAAGGGGG
1551' TCCAGGAACAATGGCAGCTTCTTGCCATCAAAAGCTGCTGATGGCACATATATTCTTAAT
** ** ** **
1551" TCCAGAAACAATGGCAGCTTCTGGCTATTAGAGCCGCTGATGGTACCTATATTCTGAAT
1621' GGTGACTACACTTTGTCCACCTTAGAGCAAGACATTATGTACAAGGTGTTGCTTGAGG
** ** **
1621" GGAAACTTCACCTCTGTCCACACTAGAGCAAGACCTCACCTACAAGGTACTGCTTAAGG
1681' TACAGCGGCTCCTCTGCGGCATTGGAAAGAAATTCGCAGCTTTAGCCCTCTCAAAGAGCCC
** ** **
1681" TACAGTGGTTCCTCGGCTGCGCTGGAAAGAAATCCGCAGCTTTAGTCCACTCAAAGAACCC
1741' TTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAATTAATAACACCTAC
** ** **
1741" TTAAACCATCCAGGTTCTTATGGTAGGCCATGCTCTCCGACCCAAATTAATTCACCTAC
1801' TTCTGTAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCAAT
** ** **
1801" TTATGAAGAAGAAGACAGAGTCATTCAACGCCATTCCACATTTTCTGAGTGGGTGAT
1851' GAGAGTGGGGCGAATGTTCTAAGTCATGTGAATGGGTTGGCAGAGAAAGACTGGTAGAA
** ** **
1851" GAGAGTGGGGGAGTGCTCCAAGACATGCGGCTCAGGTTGGCAGAGAAAGAGTAGTGCAG

F I G. 9

Hu	ADAMTS-1	1921'	TGCCGAGACATTAAATGGACAGCCCTGCTTCCGAGTGTGCAAAAGGAAGTGAAGCCAGCCAGC

Mu	ADAMTS-1	1921"	TGCAGAGACATTAAACGGACACCCCTGCTTCCGAAATGTGCAAAAGGAAGTGAAGCCAGCCAGT

		1981'	ACCAGACCTTGTGCAGACCATCCCTGCCCCCCAGTGGCAGCTGGGGGAGTGGTCAATCATGT

		1981"	ACCAGACCTTGTGCAGACCTTCCCTTGCCCCACACTGGCAGGTGGGGGATTGGTCAACCATGT

		2041'	TCTAAGACCTGTGGGAAGGGTTACAAAAGAAAGCTTGAAGTGTCTGTCCCATTGATGGA

		2041"	TCCAAAACCTTGCGGGAAGGGTTACAAGAGAAACCTTGAAATGTGTGTCCCACGATGGG

		2101'	GGGGTGTATTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTCAATAGACTTT

		2101"	GGCCTGTATTATCAAAATGAGAGCTGTGATCCTTTGAAGAAAGCCAAAGCATTACATTGACTTT

		2161'	TGCACACTGACACAGTGCAGTTAA

		2161"	TGCACACTGACACAGTGCAGTTAA

FIG. 10

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      MMP domain
Hu ADAMTS-1 1' MDICRIRLRKKRFVSSPRYVETMLVADQSM
                *****
Mu ADAMTS-1 1" EPSGPGSIRKKRFVSSPRYVETMLVADQSM

31' AEFHGSGGLKHYYLLTLFSVAARLYKHPSIRN
   * *****
31" ADFHGSGGLKHYYLLTLFSVAARFYKHPSIRN

61' SVSLVVVKILVIHDEQKGPEVTSNAALT LR
   * *****
61" SISLVVVVKILVIYEEQKGPEVTSNAALT LR

91' NFCNWQKQHNPPSDRDAEHYDTAILFTRQD
   *** *****
91" NFCSWQKQHNSPSDRDPEHYDTAILFTRQD

121' LCGSQTCDTLGMADVGTVC DPSRSCSVIED
     *****
121" LCGSHTCDTLGMADVGTVC DPSRSCSVIED
      (zinc binding
        site)
151' DGLQAAFTTAHELGHVFNMPHDDAKQCASL
     *****
151" DGLQAAFTTAHELGHVFNMPHDDAKHCASL

181' NGVNQDSHMMASMLSNLDHSQPWSPCSAYM
     *** *****
181" NGVSGDSHLMASMLSSL DHSQPWSPCSAYM

      DI domain
211' ITSFLDNGHGECLMDKPQNPIQLPGDLP GT
     *****
211" VTSFLDNGHGECLMDKPQNPIKLP SDLP GT

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F I G. 1 1

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Hu ADAMTS-1 241' LYDANRQCQFTFGEDSKHCPDAASTCSTLW
                *****
Mu ADAMTS-1 241" LYDANRQCQFTFGEE SKHCPDAASTCTTLW

271' CTGTSGGVLVCQTKHFPWADGTSCGEGKWC
      *****
271" CTGTSGGLLVCQTKHFPWADGTSCGEGKWC

301' INGKCVNKTDRKHFDTPFHGS WGPWGPWGD
      *****
301" VSGKCVNKTDMKHFATPVHGS WGPWGPWGD
                                TSP domain

331' CSRTC GGGVQYTMRECDNPVPKNGGKYCEG
      *****
331" CSRTC GGGVQYTMRECDNPVPKNGGKYCEG

361' KRVRYRSCNLEDCPDNNGKTFREEQCEAHN
      *****
361" KRVRYRSCNIEDCPDNNGKTFREEQCEAHN

391' EFSKASFGSGPAVEWIPKYAGVSPKDRCKL
      *****
391" EFSKASFGNEPTVEWTPKYAGVSPKDRCKL

421' ICQAKGIGYFFVLQPKVVDGTPCSPDSTSV
      *
421" TCEAKGIGYFFVLQPKVVDGTPCSPDSTSV

451' CVQGQCVKAGCDRIIDSKKKFDKCGVCGGN
      *****
451" CVQGQCVKAGCDRIIDSKKKFDKCGVCGGN

481' GSTCKKISGSVTSAPGYHDIVTIPTGATN
      *****
481" GSTCKKMSGIVTSTRPGYHDIVTIPAGATN

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FIG. 12

Hu ADAMTS-1 511' IEVKQRNQRGSRNNGSFLAIKAADGTYILN

 Mu ADAMTS-1 511" IEVKHRNQRGSRNNGSFLAIRAADGTYILN

541' GDYTLSTLEQDIMYKGVVLRYSGSSAALER
 * *****
 541" GNFTLSTLEQDLTYKGTVLRYSGSSAALER

571' IRSFSPLKEPLTIQVLTVGNALRPKIKYTY

 571" IRSFSPLKEPLTIQVLMVGHALRPKIKFTY

TSP domain
 601' FVKKKKESFNAIPTFSAWVIEEWGECSKSC
 * * * * *
 601" FMKKKTESFNAIPTFSEWVIEEWGECSKTC

631' ELGWQRRRLVECRDINGQPASECAKEVKPAS
 * * * * *
 631" GSGWQRRRVVQCRDINGHPASECAKEVKPAS

TSP domain
 661' TRPCADHPCPQWQLGEWSSCSKTCGKGYKK
 * * * * *
 661" TRPCADLPCPHWQVGDWSPCSKTCGKGYKK

691' RSLKCLSHDGGVLSHESCDPLKKPKHFIDF
 * * * * *
 691" RTLKCVSHDGGVLSNESCDPLKKPKHYIDF

721' CTLTQCS
 * * * * *
 721" CTLTQCS

FIG. 13

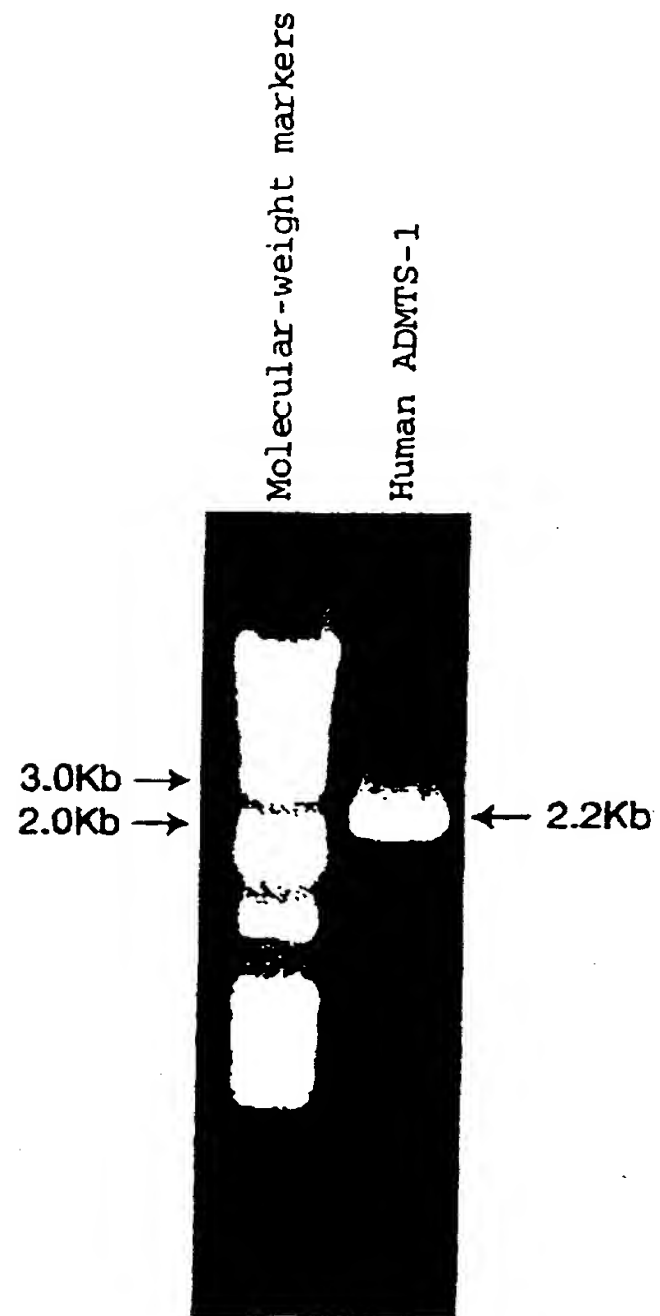


FIG. 14

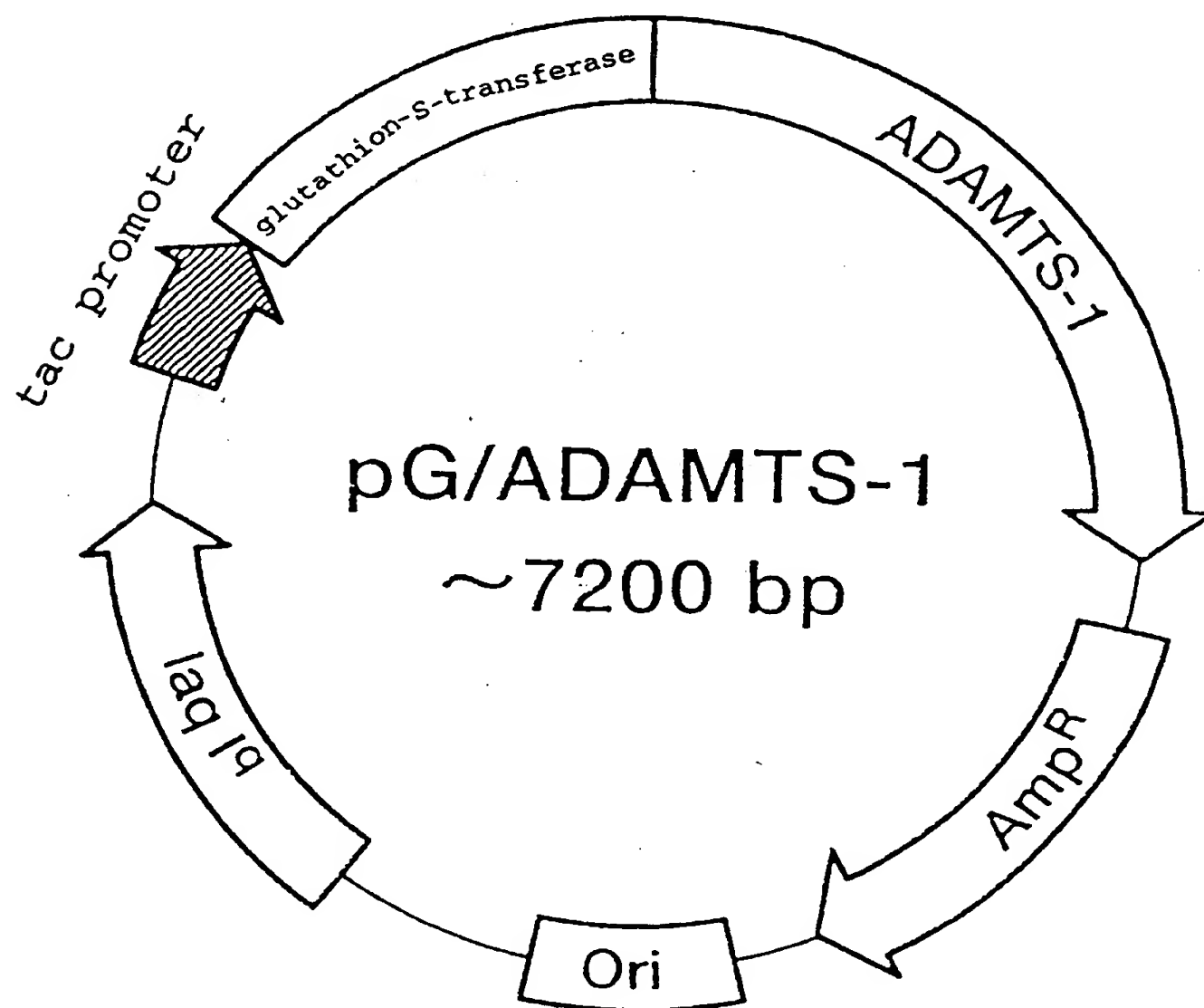


FIG. 15

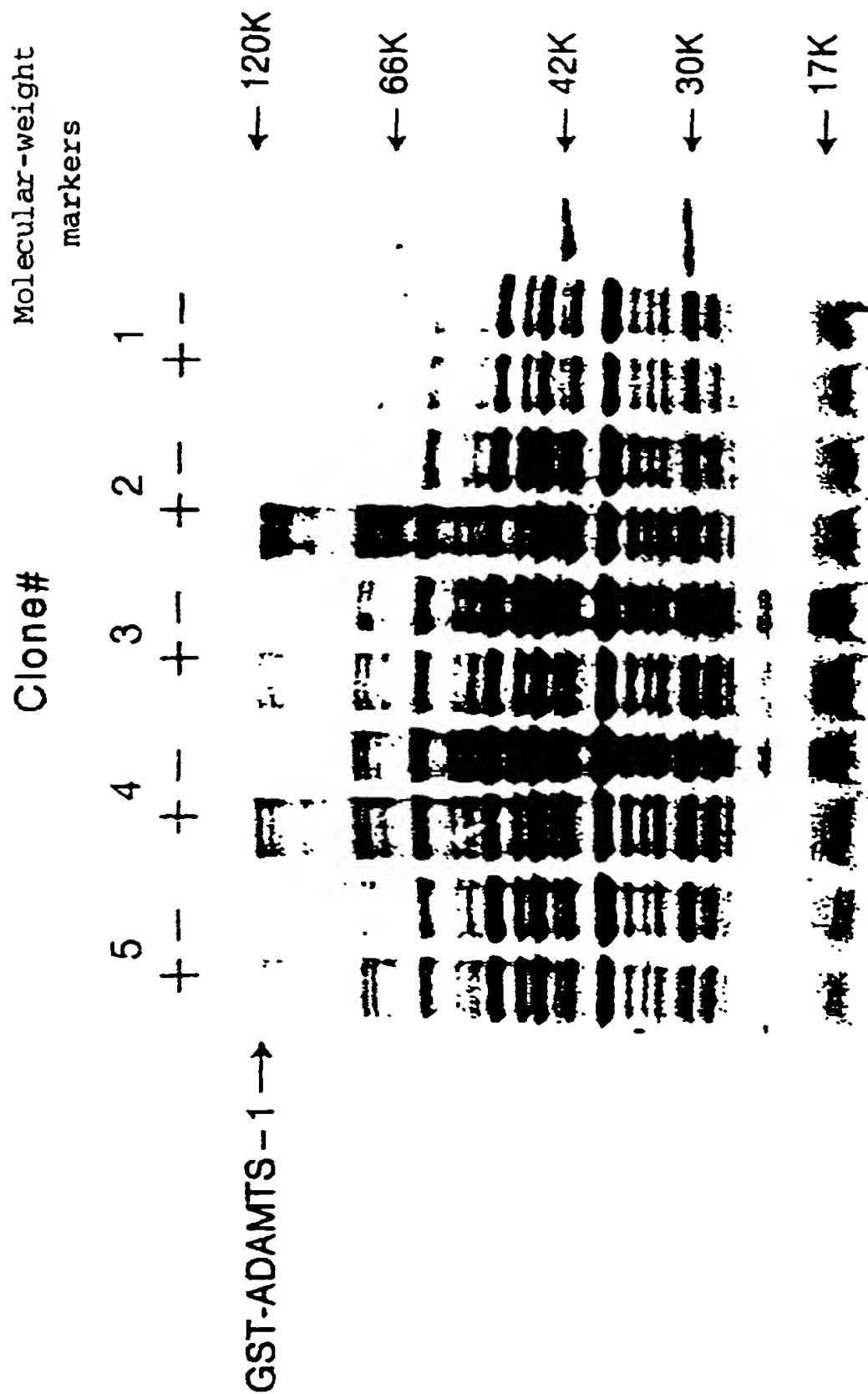


FIG. 16

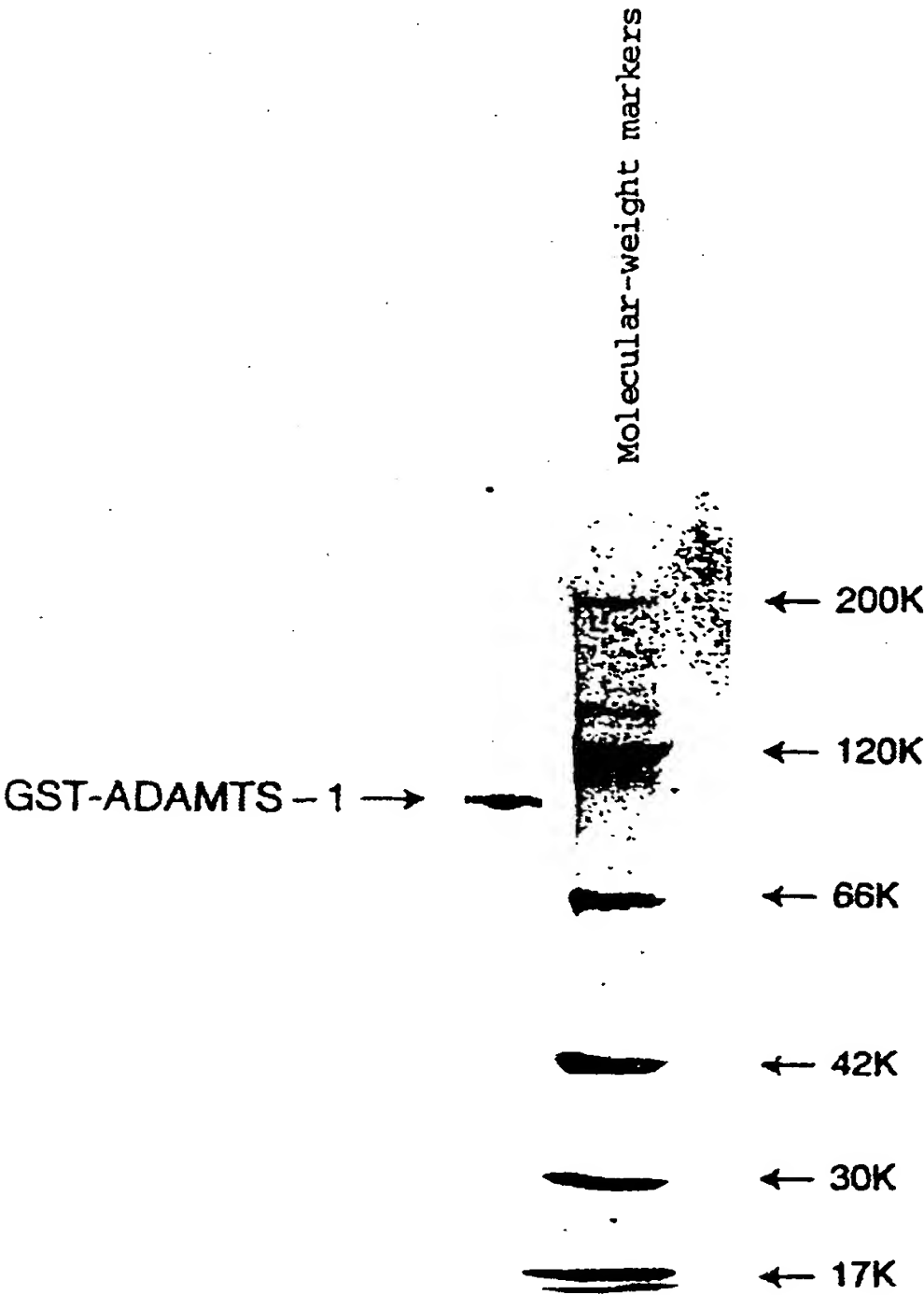
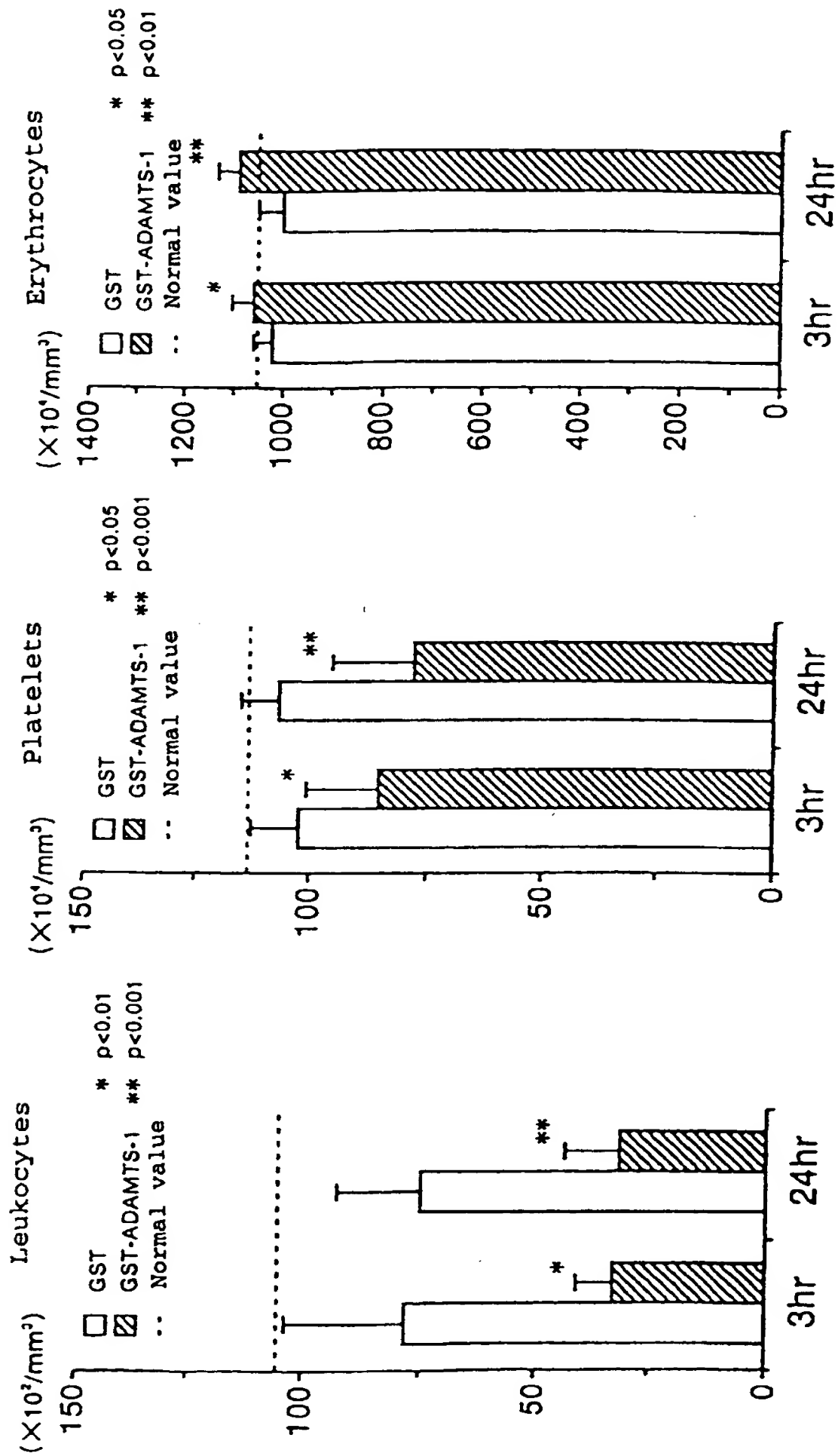


FIG. 17



INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP98/02449

A. CLASSIFICATION OF SUBJECT MATTER

Int.Cl.⁶ C12P21/02, C12N15/12, C12N1/21, A61K38/43, A61K38/48, A61K38/16, G01N33/53, A23L1/305 // C07K14/745, C07K14/78, C07K16/18,

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Int.Cl.⁶ C12P21/02, C12N15/12, C12N1/21, A61K38/43, A61K38/48, A61K38/16, G01N33/53, A23L1/305

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
SwissProt/PIR/GeneSeq, Genbank/EMBL/DDBJ/GeneSeq

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	The Journal of Biological Chemistry. Vol. 272 No. 1 (1997) Kouji Kuno et al., "Molecular Cloning of Gene Encoding a New Type of Metalloproteinase-disintegrin Family Protein with Thrombospondin Motifs as an Inflammation Associated Gene" p.556-562	1-20, 24

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance
 "E" earlier document but published on or after the international filing date
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 "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
 "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
 "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
 "&" document member of the same patent family

Date of the actual completion of the international search
4 September, 1998 (04. 09. 98)

Date of mailing of the international search report
16 September, 1998 (16. 09. 98)

Name and mailing address of the ISA/
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